

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:52:10 ; Search time 46 Seconds
(without alignments)
1803.018 Million cell updates/sec

Title: US-10-731-642A-1

Perfect score: 4534

Sequence: 1 MFLEKIVDAITGKDGKKVK.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4534	100.0	862	2 S57964	lipoxigenase (EC 1
2	3334	86.8	862	2 T07775	lipoxigenase (EC 1
3	3632.5	80.1	861	2 S44940	lipoxigenase (EC 1
4	3625.5	80.0	859	2 T06352	lipoxigenase (EC 1
5	3624.5	79.9	859	2 T06339	lipoxigenase (EC 1
6	3202.5	70.6	859	1 JQ2267	lipoxigenase (EC 1
7	3137.5	69.2	876	2 T07101	lipoxigenase (EC 1
8	2911	64.2	878	2 S74207	lipoxigenase (EC 1
9	2901	64.0	857	2 S01864	lipoxigenase (EC 1
10	2872	63.3	877	2 T10085	lipoxigenase (EC 1
11	2837	62.6	861	1 S01142	lipoxigenase (EC 1
12	2789.5	61.5	865	2 T11852	lipoxigenase (EC 1
13	2777	61.2	858	2 T12142	lipoxigenase (EC 1
14	2745.5	60.6	865	1 DAS1L1	lipoxigenase (EC 1
15	2731.5	60.2	864	1 S07075	lipoxigenase (EC 1
16	2713	59.8	862	2 S22153	lipoxigenase (EC 1
17	2693	59.4	864	2 S13381	lipoxigenase (EC 1
18	2689	59.3	856	2 T06596	lipoxigenase (EC 1
19	2686.5	59.3	853	2 T07662	lipoxigenase (EC 1
20	2685.5	59.2	853	2 T07036	lipoxigenase (EC 1
21	2680	59.1	862	2 T05941	lipoxigenase (EC 1
22	2675	59.0	868	2 T06827	lipoxigenase (EC 1
23	2660.5	58.7	839	2 T06354	lipoxigenase (EC 1
24	2660	58.7	868	2 S56555	lipoxigenase (EC 1
25	2656	58.6	839	1 DAS1L2	lipoxigenase (EC 1
26	2653.5	58.5	859	2 T05429	probable lipoxigen
27	2631	58.0	876	2 T05943	probable lipoxigen
28	2624	57.9	866	2 T06454	lipoxigenase (EC 1
29	2584.5	57.0	864	2 T05945	lipoxigenase (EC 1

30	2563	56.5	865	1 S23454	lipoxigenase (EC 1
31	2494	55.0	741	2 S18906	lipoxigenase (EC 1
32	2002.5	44.2	914	2 T07065	probable lipoxigen
33	2000.5	44.1	599	2 S18612	lipoxigenase (EC 1
34	1976.5	43.6	908	2 T07409	lipoxigenase (EC 1
35	1929.5	42.6	926	2 E96749	probable lipoxigen
36	1853	40.9	899	2 T11578	probable lipoxigen
37	1814	40.0	896	2 JQ2391	lipoxigenase (EC 1
38	1812	40.0	899	2 T07062	probable lipoxigen
39	1772	39.1	917	2 B96699	probable lipoxigen
40	1767	39.0	896	2 T07408	lipoxigenase (EC 1
41	1747.5	38.5	923	2 A53054	lipoxigenase (EC 1
42	1687	37.2	870	2 T47454	lipoxigenase AtLOX
43	1678	37.0	517	2 T06274	probable lipoxigen
44	1655	36.5	623	2 T07664	lipoxigenase (EC 1
45	1654.5	36.5	936	2 T06190	lipoxigenase (EC 1

ALIGNMENTS

RESULT 1

S57964

lipoxigenase (EC 1.13.11.12) - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: S57964

R:Veronesi, C.; Fournier, J.; Rickauer, M.; Esquerre-Tugaye, M.T.

submitted to the EMBL Data Library, January 1995

A:Description: Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA.

A:Reference number: S57964

A:Accession: S57964

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-862 <VER>

A:Cross-references: UNIPROT:Q43800; EMBL:X84040; NID:g899343; PIDN:CAA58859.1; PID:g89934

C:Superfamily: lipoxigenase

C:Keywords: oxidoreductase

Query Match	100.0%	Score 4534;	DB 2;	Length 862;
Best Local Similarity	100.0%;	Pred. No. 3.1e-296;	Mismatches 0;	Indels 0; Gaps 0;
Matches 862;	Conservative 0;			
QY	1	MFLEKIVDAITGKDGKKVGVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLEISSV	60	
DB	1	MFLEKIVDAITGKDGKKVGVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLEISSV	60	
QY	61	NADPANGIQQKRSKAAYLENMLTNSPTIAAGSAPRVTFDWDDEBFGVPGAFIKNLHFS	120	
DB	61	NADPANGIQQKRSKAAYLENMLTNSPTIAAGSAPRVTFDWDDEBFGVPGAFIKNLHFS	120	
QY	121	EFPLKSLTLEDVPHNGKHVFCVNSWVYPANKYKSDRIIFANQAYLPSETPTDLRKYRENE	180	
DB	121	EFPLKSLTLEDVPHNGKHVFCVNSWVYPANKYKSDRIIFANQAYLPSETPTDLRKYRENE	180	
QY	181	LVTLRGDTGKLEEDRVYDYAYNDLGDPPKQDLSPVLCGSSEYYPVPRGRTRKPT	240	
DB	181	LVTLRGDTGKLEEDRVYDYAYNDLGDPPKQDLSPVLCGSSEYYPVPRGRTRKPT	240	
QY	241	KTDPNSESRIPLMLSDIYVPRDERFGHILKSDFTLTFALKSTIVQLLPEFKALFDSTHNE	300	
DB	241	KTDPNSESRIPLMLSDIYVPRDERFGHILKSDFTLTFALKSTIVQLLPEFKALFDSTHNE	300	
QY	301	FDSFEDVLKVEGGIKLPQGPLLKAITDSIPLEIILKELLRSDEGLFKYPTPQVQEDKT	360	
DB	301	FDSFEDVLKVEGGIKLPQGPLLKAITDSIPLEIILKELLRSDEGLFKYPTPQVQEDKT	360	
QY	361	AWRTDEEFGREMLAGVNPVILSRLOEFPKSLDKPIYGNQNSTITREIQIEDKGLTLD	420	
DB	361	AWRTDEEFGREMLAGVNPVILSRLOEFPKSLDKPIYGNQNSTITREIQIEDKGLTLD	420	
QY	421	BAIKTNRLFIINHHIDILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHPD	480	

Db 421 EAIKTNRLFILNHHDLMPYLRINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHD 480
Qy 481 GDQFQAVSVYTPADQGVGSIWQAKAYAAVNDGSGVHQLISHWLNTHAAIEPFFVIATNR 540
Db 481 GDQFQAVSVYTPADQGVGSIWQAKAYAAVNDGSGVHQLISHWLNTHAAIEPFFVIATNR 540
Qy 541 QLSALHPIYKLLHPHFRMTNINARQILINGGGELLEITVFPKYSMEMSAVVYKDWVF 600
Db 541 QLSALHPIYKLLHPHFRMTNINARQILINGGGELLEITVFPKYSMEMSAVVYKDWVF 600
Qy 601 PQOALPTDLIKRGVAVEDSSPLGIRLLIQQDYPAVDGLKIWSAISKSWTEYCNYYKSD 660
Db 601 PQOALPTDLIKRGVAVEDSSPLGIRLLIQQDYPAVDGLKIWSAISKSWTEYCNYYKSD 660
Qy 661 DAVQKDTTELQAWKELREBEGHGDKDEPWWPKQVTVQELIDSCITTIWIASALHAAVNF 720
Db 661 DAVQKDTTELQAWKELREBEGHGDKDEPWWPKQVTVQELIDSCITTIWIASALHAAVNF 720
Qy 721 QYPAAGYLPNRPRTLNRNFMPEPGSPYEELKTNPKVFLKTTIPQOLTLGLSLIEILSR 780
Db 721 QYPAAGYLPNRPRTLNRNFMPEPGSPYEELKTNPKVFLKTTIPQOLTLGLSLIEILSR 780
Qy 781 HSSDLYLGQRESPEWTQDQPLSAPARFGKKLSIEDQIMQMVNDKWKNSRSGPVKPY 840
Db 781 HSSDLYLGQRESPEWTQDQPLSAPARFGKKLSIEDQIMQMVNDKWKNSRSGPVKPY 840
Qy 841 TLLFPTSEGGLTGKIPNSVSI 862
Db 841 TLLFPTSEGGLTGKIPNSVSI 862

RESULT 2
T07775
lipoxigenase (EC 1.13.11.12) LX-3 - potato
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07775
R:Kolomiets, M.V.; Hannapel, D.J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z16124
A:Accession: T07775
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-862 <KOL>
A:Cross-references: UNIPROT:Q43191; EMBL:U60202; NID:G1407704; PIDN:AAB67865.1; PID:G140
A:Experimental source: cv. Berolina
C:Genetics:
A:Gene: LX-3
C:Function:
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis, cis per
C:Superfamily: lipoxigenase
C:Keywords: fatty acid oxidation; oxidoreductase

Query Match 86.8%; Score 3934; DB 2; Length 862;
Best Local Similarity 85.1%; Pred. No. 6.1e-256;
Matches 735; Conservative 64; Mismatches 61; Indels 4; Gaps 3;

Qy 1 MFLEKIVDAITGK--DDGKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVSLLEIS 58
Db 1 MLEKIVEAISGRSEBNGKKVGTIVLMKKNVLDFTDINASVLDGVLEFLGRRVSLQLIS 60

Qy 59 SYNADPANGCLOCKRSKAAVLEWLNSTPIAGESAFTVFDWDEEGVPGAFIINKLH 118
Db 61 VHADPGNSLQCKRNPAYLEKWLATGTSLVAGESAFDVTFDW-DEDIGVPGAFIINNPH 119

Qy 119 FSEFFLKSITLEDVFNHGVHVCNWSVYPANKYKSDRIFFANQAYLPSETPTLTKVRE 178
Db 120 FNEFYKSLITLEDVFNHGVHVCNWSVYPANKYKSERIFFANQAYLPGETEPLNRYE 179

Qy 179 NELVTLRGDTGKLEBWDVRYAYYNDLGDPKQDLSRPVLGSGSEYPPYPRGRTRK 238
Db 180 KELVNLRGNGKLEBWDVRYAYYNDLGDPKQDLSRPVLGSGSEYPPYPRGRTRK 239

Qy 239 PTKTDPNSESRIPLMLSDIYVPRDERFGHTKLSDFELTALKSIVQLLLPEFKALFDSTH 298
Db 240 PTKADPKSESRIPLMLSDIYVPRDERFGHTKLSDFELTALKSIVQLLLPEFKALFDSTP 299
Qy 299 NEFDSFEDVLKLYEGGIKLPQGPLLKAITDSIPLEILKELLARSDEGLFKYPTPQVIOED 358
Db 300 DEFDSFEDVLKLYEGGIKLPQGPLLKAITDSIPLEILKELLARSDEGLFKYPTPQVIOED 359
Qy 359 KTAWRTEDEFGREMLAGVNPVVISRLQEPFKSKLDPKIYQNSSTITREQIEDKLDGLT 418
Db 360 KSSWRTDEEFAREMLAGVNPVVISRLQEPFKSKLDSEVYQNSSTITKEHIENTDGLT 419
Qy 419 IDEAKTNRLFILNHHDLMPYLRINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPH 478
Db 420 IDDAKTNRLYILNHHDLMPYVRINT-TNKUYASRTLLFLQDNGTGMKPVALIELSLPH 478
Qy 479 PDGQFQAVSVYTPADQGVGSIWQAKAYAAVNDGSGVHQLISHWLNTHAAIEPFFVIAT 538
Db 479 PDGDELGAHSVSVYTPADQGVGSIWQAKAYAAVNDGSGVHQLISHWLNTHAAIEPFFVIAT 538
Qy 539 NRQLSALHPIYKLLHPHFRMTNINARQILINGGGELLEITVFPKYSMEMSAVVYKDW 598
Db 539 NRQLSVLHPIHKLHPHFRMTNINARQILINAGGVLEMTVFPKAYAMEMSAVVYKSW 598
Qy 599 VFPEQALPTDLIKRGVAVEDSSPLGIRLLIQQDYPAVDGLKIWSAISKSWTEYCNYYK 658
Db 599 VFPEQALPADLIKRGVAVEDSSPHGVLLLIQQDYPAVDGLKIWSAISKSWTEYCNFYK 658
Qy 659 SDDAVQKDTTELQAWKELREBEGHGDKDEPWWPKQVTVQELIDSCITTIWIASALHAAVN 718
Db 659 SDELVLKQNELQAWKELREBEGHGDKDEPWWPKQVTVQELIDSCITTIWIASALHAAVN 718
Qy 719 FGQYPAAGYLPNRPRTLNRNFMPEPGSPYEELKTNPKVFLKTTIPQOLTLGLSLIEIL 778
Db 719 FGQYPAAGYLPNRPRTLNRNFMPEPGSPYEELKTNPKVFLKTTIPQOLTLGLSLIEIL 778
Qy 779 SRHSDDTLYLQGRESPEWTQDQPLSAPARFGKKLSIEDQIMQMVNDKWKNSRSGPVK 838
Db 779 SRHASDEIYLGQRESSEWTQDQPLAFAFERFGKKLSEIEDQIQNGDKKWKNSRSGPVN 838
Qy 839 PYTLFPTSEGGLTGKIPNSVSI 862
Db 839 PYTLFPTSEGGLTGKIPNSVSI 862

RESULT 3
S44940
lipoxigenase (EC 1.13.11.12) - potato
C:Species: Solanum tuberosum (potato)
C:Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S44940
R:Casey, R.
submitted to the EMBL Data Library, May 1994
A:Reference number: S44940
A:Accession: S44940
A:Molecule type: mRNA
A:Residues: 1-861 <CAS>
A:Cross-references: UNIPROT:P37831; EMBL:X79107; NID:G486618; PIDN:CAA55724.1; PID:G48661
A:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 80.1%; Score 3632.5; DB 2; Length 861;
Best Local Similarity 78.9%; Pred. No. 1.1e-235;
Matches 672; Conservative 83; Mismatches 95; Indels 3; Gaps 3;

Qy 12 GKDDKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISSVADPANGLOCK 71
Db 12 GHDDSKVKGTVVMMKNVLDFTDLAGSLTGKIFDVLGQKVSFQLISSVQGDPTNGLQK 71

Qy 72 RSKAAYLENWLTNSTPIAAG-ESAPRVTFDWDDEFGVPGAFIINKLHFSFEFLKSLTLE 130
Db 72 HSNPAYLENLFTLTPLTAGSETAFGVTFDW-NBEFVGPGAFIINKMHINEFFFLKSLTLE 130

Query Match	80.0%	Score 3625.5	DB 2	Length 859
Best Local Similarity	79.4%	Pred. No. 3.2e-235		
Matches 685	Conservative 70	Mismatches 103	Indels 5	Gaps 3
Qy	1	MFLEKIVDAITGDKDGGKVKGTGTVLMKKNVLDFTDINASVLDGVLFGRVLSLELIS-S	59	
Db	1	MSLGGIVDAITGDKDGRPKVKGRVILMKKNVLDFTINIGASVVDGIGDILGQKVSQILISGS	60	
Qy	60	VNADPANGLOCKERSKAAYLENMLTNSPTIAAGSSAFRVTFDWDDEEFGVPGAFIINKLHF	119	
Db	61	VNYD--GLEGKSLNPAYLESWLTDTPTITAGESTTSVTFDWRDFGVPGAFIINKLHL	117	
Qy	120	SEFPLKSLTLEDVPHGKHVFCVNSVYPANKYKSDRIFFANQAYLPSEPDTLRKVKREN	179	
Db	118	NEFPLKSLTLEDVPHGKHVFCVNSVYPANKYKSDRIFFANQAYLPSEPDTLRKVKREN	177	
Qy	180	ELVTLRGDGTGKLEEDRWVYDAYYNDLGDPPDKGQDLSRPVLGSGSSEYPYPRRGRTGRKP	239	
Db	178	ELVALRGDGTGKLEEDRWVYDAYYNDLGDPPDKGQDLSRPVLGSGSSEYPYPRRGRTGRKP	237	
Qy	240	TKYTDPNSESIPLMLSLDIYVPRDERFGHIKLSDFITFALKSVTLQVLLPBFKALFPOSTHN	299	
Db	238	TKADPNCESENPLMSLDIYVPRDERFGHVKSGDFTLSLKSLSQTLPLPAFKALCDNTPN	297	
Qy	300	EFOSFEDVLKYEGGIKLQGPILLKAITDSIPLSEILKELLARSDEGLFKYPTQVQIODEK	359	
Db	298	EFNSFADVLNLYEGGIKLPEGPWLKAITNISSEIILKIDLOTQDQGLLYKPTPQVTOGDK	357	
Qy	360	TAMRTDEEFGREMLAGVNPVVISRLQBFPPKSKLDPKIYGNQNSTITREQIEDKLQGLTI	419	
Db	358	TAMRTDEEFGREMLAGSNPVLISRLQBFPPKSKLDPTIYGNQNSTITTEHVQDKLGLTV	417	
Qy	420	DEAIKYNRLFILNHHDIIMPYLRINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHP	479	
Db	418	NEAIKSNRLFILNHHDIYVPLLRKINMSANTKAYASRTLLFLQDDRTLKPLAIELSLPHP	477	
Qy	480	DGDOFGAVSKVYTPADQGVGSGTQWLAKAYAAVNDGSGVHQLISHWLNTHAAIEPFFVIATN	539	
Db	478	DGDOFGTVSKVYTPADQGVGSGTQWFAKAYAVNDMGIIHQLISHWLNTHAAIEPFFVIATN	537	
Qy	540	QLSALHPIYKLLHPHFRETMTNALARQILINGGGILLELTVPFPAKYSMEMSAVYKDWV	599	
Db	538	RHLSVLHPHKLHPHFRTMTNALARETLTYDGG-FETSLFPAPKYSMEMSAAYKDWV	596	
Qy	600	FPOQALPTDLIKGVAVESSSPGLRLLIODYPYAVDGLKIWSAIXSWTVEYCNYYKS	659	
Db	597	FPEQALPADLLKGVAVEDESSPHGRLLIIDLPPYAVDGLLEIWSAIXSWTVEYCKFYKS	656	
Qy	660	DDAVQDTELQAWKKELRREGHGDKDEPWPQKWQVQELIDSCCTITIMIASALHAAVNF	719	
Db	657	DETVKDELQAWKKELRREGHGDKDEAWPKLQTRQELURDCCTIIIMIASALHAALHF	716	
Qy	720	GQPYAGYLPNRPRTLGRNFMPEGSPGEYBELKTNPKVFLKTTIPLOQLTLGSLISLEIS	779	
Db	717	GLXSYAGYLPNRPRTLSCNLMPEGSGVEYELKTNPKVFLKTFVPQLQSILLEISIFEVSS	776	
Qy	780	RHSDTLYLGQRESPPWTQDQEPISAPAFPGKLSIDIEQIOMQNVNDEKWNKSGPVKVP	839	
Db	777	RHASDEVYLGQSDSIIEWTKDKEPLVAFERFGKMLSDIENRIMMNGHKSQKNRSGPVNVP	836	
Qy	840	YTLTLFPTSEGLTGKGI PMSVSI 862		
Db	837	YTLTLFPTSEGLTGKGI PMSVSI 859		

RESULT 5

T06339

lipoxigenase (EC 1.13.11.12) loxB - tomato

C:Species: Lycopersicon esculentum (tomato)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C:Accession: T06339

R:Perrie, B.J.; Beaudoin, N.; Burkhardt, W.; Bowsher, C.G.; Rothstein, S.J.

Plant Physiol. 106, 109-118, 1994
A:Title: The cloning of two tomato lipoxygenase genes and their differential expression
A:Reference number: Z15612; MUID:95062736; PMID:7972514
A:Accession: T06339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-859 <FER>
A:Cross-references: UNIPROT:P38416; EMBL:U09025; NID:G575431; PIDN:AAA53183.1; PID:G4829
A:Experimental source: strain Caruso; tissue-type fruit pericarp
C:Genetics:
A:Gene: loxB
C:Superfamily: lipoxygenase
C:Keywords: oxidoreductase

Query Match 79.9%; Score 3624.5; DB 2; Length 859;
Best Local Similarity 79.3%; Pred. No. 3.7e-235;
Matches 684; Conservative 71; Mismatches 103; Indels 5; Gaps 3;
QY 1 MFLEKIVDAITGKDDGKVKGTVMVLMKNVLDFTDINASVLDGVLEFLGRVSVLELIS-S 59
DB 1 MSLGGIVDAIIGKDRPKVKGRVLMKNVLDFTINIGASVVDGSDLLGQKVSQISGS 60
QY 60 VNADPANGLOGKRSKAAYLENWLNTSTPIAAGESAFRTVFDWDDDEFGVPGAFIKNLHF 119
DB 61 VNYD--GLECKSNPAYLESWLTDITITAGESTFSTFDWDRDERGCVPGAFIKNLHL 117
QY 120 SEFFLKSITLEDVPHNGKVFVCSNWVYPANKYKSDRIFFANQAYLPSETPTDTRKYREN 179
DB 118 NEFFLKSITLEDVPHNGKVFVCSNWVYPANKYKSDRIFFANQAYLPSETPTDTRKYREN 177
QY 180 ELAVTLRGDGTGLKEWDVRYVAYVNDLGDGPKGDLSPVLGSGSEVYPYPRGRGTGRK 239
DB 178 ELVLRGDTGLKEWDVRYVAYVNDLGDGPKGDLSPVLGSGSEVYPYPRGRGTGRK 237
QY 240 TKTDPNSSSRIPLLMSLDIYVPRDERFGHILKSLDFTLPAKLSIQLLLPEKALFDSTHN 299
DB 238 TKADNCSRNPLMSLDIYVPRDERFGHVKSDFTLSSLSKSIQTLPAFKALCNDTPN 297
QY 300 EFDSPEDVLKYEIGIKLPOGPLLKAITDSTIPLKELKLSRDEGLPKYPTPOVIOBQDK 359
DB 298 EFNSPADVNLNLYEGGIKLEPGFWLKAITDNTSSEILKDIQLDQGGGLKLYPTPOVIOBQDK 357
QY 360 TAWRTDEEFGREMLAGVNPVILSRLOEPPPKSLDPKLYGNQNSTITREQIEDKLDGTLTI 419
DB 358 TAWRTDEEFGREMLAGVNPVILSRLOEPPPKSLDPKLYGNQNSTITTEHVQDKLNGTLV 417
QY 420 DEAIKTNRLFILNHHDIIMPYLRLINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPH 479
DB 418 NEAIKSNRLFILNHHDIIMPYLRLINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPH 477
QY 480 DQDQFGVSKVYTPADQGVGSIWOLAKAYAVNDGSGVHQLISHWLNTHAAIEPPVIATN 539
DB 478 DQDQFGVSKVYTPADQGVGSIWOLAKAYAVNDGSGVHQLISHWLNTHAVIEPPVWATN 537
QY 540 ROLSAHPYKLLHHPHRETMINALAQILINGGGLLELTVPFPAKYSWMSAVVYKDW 599
DB 538 RHLVSLVHPHILHHPHRETMINALARETLTYDGG-FETSLFFPAKYSWMSAAAYKDW 596
QY 600 FPEQALPDLIKRGVAVEDSSPLGIRLLIODYPVAVDGLKIWSAIAKSWVTEYCNYYKS 659
DB 597 FPEQALPADLLKRGVAVEDSSPHGIRLLIILDPYAVDGLLEIWAIAKSWVTEYCKFYKS 656
QY 660 DDVOKOTELQAWKELREBEGDKKDEPPWPKMQTVQELIDSCITTIWIASALHAANVP 719
DB 657 DETVEKOTELQAWKELREBEGDKKDEAWPKLQTRQELRDCCTIIWIASALHAALHF 716
QY 720 GOYPVAGVLPNRPPLSRNMPPEGSPVEELKTNPKVFLKTTIPQLQTLGLSILELTS 779
DB 717 GLYSVAGVLPNRPPLSRNMPPEGSPVEELKTNPKVFLKTTIPQLQTLGLSILELTS 776
QY 780 RHSDSTLYLGQRESPEWTKDQPLSAFARFGKLSIEDQIMQNVDBKWNRSRGPVKVP 839
DB 777 RHASDEVYLGQDSIEWTKDEPLVAERFGQMLSDIENRIMIMNSHKSWNRSRGPVNV 836

QY 840 YTLFLPTSEGLTCKGIPNSVSI 862
DB 837 YTLFLPTSEGLTCKGIPNSVSI 859
RESULT 6
QJ02267
lipoxygenase (EC 1.13.11.12) Lox1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JQ2267
R:Melan, M.A.; Dong, X.; Endara, M.E.; Davis, K.R.; Ausubel, F.M.; Peterman, T.K.
Plant Physiol. 101, 441-450, 1993
A:Title: An Arabidopsis thaliana lipoxygenase gene can be induced by pathogens, abscisic
A:Reference number: JQ2267; MUID:94105302; PMID:7506426
A:Accession: JQ2267
A:Molecule type: mRNA
A:Residues: 1-859 <MEL>
A:Cross-references: UNIPROT:Q06327; GB:L04637; NID:G289202; PIDN:AAA32827.1; PID:G289203
C:Comment: This enzyme catalyzes the hydroperoxidation of polyunsaturated fatty acids cor
C:Superfamily: lipoxygenase
C:Keywords: fatty acid oxidation; oxidoreductase
Query Match 70.6%; Score 3202.5; DB 1; Length 859;
Best Local Similarity 68.7%; Pred. No. 8.2e-207;
Matches 595; Conservative 122; Mismatches 138; Indels 11; Gaps 7;
QY 1 MFLEKIVDAITG---KDDGKKVKGTVMVLMKNVLDFTDINASVLDGVLEFLGRVSVLELI 57
DB 1 MFGELRDLTGGGNETTTTKVKGTVMVLMKNVLDFTDNASFLDLRLEFLGNKITRLV 59
QY 58 SSVNADPANGLOGKRSKAAYLENWLNTSTPIAAGESAFRTVFDWDDDEFGVPGAFIKNL 117
DB 60 SSDVTDSENGSKGLKAAHLEDWITITSLTAGESAFKVTFDY-ETDGFYPGAFILNS 118
QY 118 HFSFEFLKSITLEDVPHNGKVFVCSNWVYPANKYKSDRIFFANQAYLPSETPTDTRKYR 177
DB 119 HFSFEFLKSITLEDVPHNGKVFVCSNWVYPANKYKSDRIFFANQAYLPSETPTDTRKYR 178
QY 178 ENELVTLRGDGTGLKEWDVRYVAYVNDLGDGPKGDLSPVLGSGSEVYPYPRGRGTGR 237
DB 179 EELVSLRGDTGEGELKEWDVRYVAYVNDLGVPPKN--PRPVLGGTQEVYPRGRGTGR 235
QY 238 KPTKTDPNSSSRIPLLMSLDIYVPRDERFGHILKSLDFTLPAKLSIQLLLPEKALFDST 297
DB 236 KPTKEDPQTSRLSPITSSLDIYVPRDERFGHILKSLDFTLPAKLSIQLLLPEKALFDST 295
QY 298 HNEFDSFEDVLKLYEGGIKLEPGFWLKAITDSTIPLKELKLSRDEGLPKYPTPOVIOE 357
DB 296 KPEFDSFEDVLKLYEGGIKLEPGFWLKAITDSTIPLKELKLSRDEGLPKYPTPOVIOE 355
QY 358 DKTAWRTDEEFGREMLAGVNPVILSRLOEPPPKSLDPKLYGNQNSTITREQIEDKLDGL 417
DB 356 DKTAWRTDEEFGREMLAGVNPVILSRLOEPPPKSLDPKLYGNQNSTITREQIEDKLDGL 415
QY 418 TIDRAIKTNRLFILNHHDIIMPYLRLINTSDTKTYASRTLLFLQDNGTLKPSAIELSLP 477
DB 416 TVEALKEKRLFILNHHDIIMPYLRLINTSDTKTYASRTLLFLQDNGTLKPSAIELSLP 474
QY 478 HPDQDQFGVSKVYTPADQGVGSIWOLAKAYAVNDGSGVHQLISHWLNTHAAIEPPVIA 537
DB 475 HPNGDKFGVSEVYTPG-EGVYDSLWQLAKAFVGNDSGNHQLISHWLNTHAAIEPPVIA 533
QY 538 TNRLQSLALHPYKLLHHPHRETMINALAQILINGGGLLELTVPFPAKYSWMSAVVYKDW 597
DB 534 TNRLQSLVLPVFKLLEPHFRDTRMINALAQILINGGGLLELTVPFPAKYSWMSAVVYKDW 593
QY 598 -WPEQALPDLIKRGVAVEDSSPLGIRLLIODYPVAVDGLKIWSAIAKSWVTEYCNYY 656
DB 594 HWTTPDQALPAELKRGVAVEDPEAPHLRLIKDYPYAVDGLGLEVWYIAESWVRDIYFLF 653
QY 657 YKSDDAVQKOTELQAWKELREBEGDKKDEPPWPKMQTVQELIDSCITTIWIASALHAA 716

[illegible]

RESULT 7
T07101
lipoxigenase (EC 1.13.11.12) - potato
C:Species: Solanum tuberosum (potato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07101
R:Basso, B.; Giribaldi, G.; Sironi, G.; Mizzi, L.M.; Righi, M.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z15920
A:Accession: T07101
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-876 <BAS>
A:A:Cross-references: UNIPROT:Q14130; EMBL:U24232; NID:g1117792; PIDN:AAD09202.1; PID:g1117792
C:Genetics:
A:Introns: 79/1; 173/3; 254/1; 368/3; 397/3; 433/3; 535/2; 623/1
C:Function:
A:Description: catalyzes the peroxidation of polyunsaturates fatty acids to their corres
C:Superfamily: lipoxigenase
C:Keywords: fatty acid oxidation; iron; oxidoreductase

Query Match	69.2%	Score	3137.5;	DB	2;	Length	876;
Best Local Similarity	66.9%;	Pred.	No. 2e-202;				
Matches	591;	Conservative	119;	Mismatches	142;	Indels	31;
Gaps	10;						
QY	3	LKXIVDAITCKD-----	DGKKVGTGVVLMEKNVLDFTDINASVLVDGVLEF	47			
DB	2	LKWLDVVOCGKNNDITDENNCNNIHNGKKVGTVLMBEECLDLTNVGASLLDRPHEV	61				
QY	48	LGRVSLELTSSVNADPANGLQGKRSAAYLENWLNTSTPIAAGESAFRVTTFDWDDEFG	107				
DB	62	IGKVSLQLISADHAE-P--CCTGKLGPFALEKWIWISTLTLSISAGDATFNWTFDW--DES MG	118				
QY	108	VPGAFIIXNLFHSFEFLKSJLTLEDVPNHGKHVFVCNSWVYPANKYKSDRIFFANQAOLPS	167				
DB	119	VPGAFIIXNVHHQSQFYLRITVLEDDVPCHGELHFVCNSWVYPAHRYKYDVRFVFFANKTYLPS	178				
QY	168	ETPDTRKRENELVTLRGDTGKLEBWDVVYAYYNDLGDPPKGODLSRPVLGGSEY	227				
DB	179	NTEPLRPYREQELLRLSGSGSKLKEDWRVYDYRFYNDLGFPDKGDPYVVRPVILGGSKEY	238				
QY	228	PYPRRGTRCKPKPT---DNSSSRIPLLMSLDIYVPRDERFRGHIKLSDFLTPALKSIQV	284				
DB	239	PYPRRGTSRRATKTGFADPMSESRLPPL--GLDIYAPRDERFTPVKUSDIFLAYAVKSLQG	297				
QY	285	LILPEFKALFDSTHNEPDSFEDVKLYEGGIKLPQGPLLKAITDSIPLEILKELLRS DGE	344				
DB	298	VLIPEIAALFDKTIINEFDNFEDVKLYEGGIKLPDHH-LKKLRQCIPWEMKELVRS DGE	356				
QY	345	GLPKYPTPQVIOBKTAWRTDDEFGRMLAGVNPVIISRLOEPPPKSLDPKIYGQNOST	404				
DB	357	PFLKFMPMDVIKVDRSAWRTDEREFGRMLAGVNPVIIRRLQEPPPAKSLDPVEYGNQTSS	416				
QY	405	ITREQIEDKDGUTIDBAIKTNRLFILNHHIDLMPYLRRINTSTDTKTYSARTLLFLLODN	464				
DB	417	KREHIEXKMMDGLTVDEAIECNRLFILDHHDALLPYLRRINT-TKTKYTATRLLLYLODN	475				

[illegible]

RESULT 8
S74207

lipoygenase (EC 1.13.11.12) - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S74207; S74137
R:Hoehne, M.; Nellen, A.; Schwennessen, K.; Kindl, H.
Eur. J. Biochem. 241, 6-11, 1996
A:Title: Lipid body lipoygenase characterized by protein fragmentation, cDNA
A:Reference number: S74137; MUID:97054584; PMID:8898881
A:Accession: S74207
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <HOE>
A:Cross-references: UNIPROT:Q42710; EMBL:X92890; NID:G1296511; PIDN:CAA63483.1
A:Experimental source: tissue cotyledones, clone PCSLBLOX221
A:Accession: S74137
A:Molecule type: protein
A:Residues: 136,'X',198-204;218,'FX',221-223,'XX',226-228;305-309,'XX',312-316
C:Superfamily: lipoygenase
C:Keywords: oxidoreductase

Query Match	64.2%;	Score 2911;	DB 2;	Length 878;
Best Local Similarity	62.3%;	Pred. No. 3.2e-187;		
Matches 534;	Conservative 140;	Mismatches 175;	Indels 8;	Gaps 6
Qy	6	IVDAITGDKDGKVKGTWLMKKNVLDFDTDINASVLGVLFGFGRVRSLELISSVYNADPA	65	
Db	30	ILDRVSSL-GGNKIKGKIVLMRSNVNLFDTFPHSNLLDNFTLLGGGVFQLISATHT--S	86	
Qy	66	NLGQGRKSKAAYLENWLTNSTPIAAGESAPRVVTFDWDDEEFGVPGAFIKNLHFSEFFLK	125	
Db	87	NDSRGKVGKNKAYLERWLTSIPPLFAGESVFGINFQW--DENEGFGPAPFIKNGHTSEFFLK	145	
Qy	126	SLTLEDVPMHGKVFVNCNSWVYPANKYKSORIIFANQAYLPSEPTDRLKRYRENELVTLR	185	
Db	146	SLTLDDVFGYGRVHFDCNSWYPSGRYKOKRIFFANHVLYLPSQTNPRLURKRYREBELWNLR	205	
Qy	186	GDGTGLKEEDRWVVDYAYNDLGDPPDXGQDLRRPVLGSSSSYPYPRRGRTGRKPTKTDPN	245	
Db	206	GDGTGERKEWDRIVDYVDYNDIADPDVGD--HRPILGTTTEVPYPRRGRTGRPSRRDHN	263	
Qy	246	SEGRIPLLMSLDIYVPRDERFGHTKLSDFTLTFALKSIVQLLLPFKALFDSTHNEFDSE	305	

Query Match	62.6%	Score 2837	DB 1	Length 861
Best Local Similarity	61.4%	Pred. No. 2.9e-182		
Matches 534	Conservative 138	Mismatches 168	Indels 30	Gaps 10
QY	10	ITG-KDGGKVKGTGVLMKKVNLDF-----DINASVLDDGVLEFLEGRVSLSE	55	
Db	5	VTGILNRGHKIKGTVMNRKNVLDINSLTTVGVGIGQGFILGSTVDNLTAFIGRSVSLQ	64	
QY	56	LISVSNADPANGILOGKRSKAAAYLENWLNTSTPIAAGESAPRVFTFDWDEBFGVPGAFI	115	
Db	65	LISATKPD-ATG-KGKLGKATFLEGIISLPTLGCAGSAFKHFEDWD-DMGIPGAFYIK	121	
QY	116	NLHFSSEFFKSLTLEDVPHNGKVHFCVNSWVPYANKYKSDRIFPAQYALPSETPTL	175	
Db	122	NFMQTEFFVLVSLTDDIPNHGSIYFVCNSWYNAKHKIDRIFFANQYVLPSETPA	181	
QY	176	YREVELVTLRGDTGKLEWDRVVDYAYNDLGDPPKQDLSRPVLGGSESYPPRRGRT	235	
Db	182	YREEELNNLRGDTGRKEWERIYDVTVDNLGNPDGSENHARPVLGGSSTYPPRRGRT	241	
QY	236	GRKPTKTDNSESRIPLMLSLDITVYRDRERFEGHILKSLDTFALKSIIVOLLPEFKALF	294	
Db	242	GRKPTRKDNSESRIPLMLSLDITVYRDRERFEGHILKSLDTFALKSIIVOLLPEFKALF	296	
QY	295	--DSTHNEFSDFDVLKYEYGGIKLPQGGKALKAITDSIPLLEILKELRSDEGLFKYPT	352	
Db	297	DLNFTNEFSDFDVHGLYEGGIKLPN-ILSQIS--PLPVLKEIFRTDGTENTLYKPPP	352	
QY	353	QVIQEDKTAWRTDEEFGREMLAGVNPVVISRLQEPFPPKSLDPKIVGNQNSTITRQ	412	
Db	353	KVIQVRSRGWMTDEEPAREMLAGVNPVICCLQEPFPPKSLDSQIYGDHTSKISKEHLEP	412	
QY	413	KLDGLTIDRAIKTNRLFIILNHHDLIMPYLRRINTSTDTKTYASRTLLFLQDNGTILKPSAI	472	
Db	413	NLEGLTVEEAIQNKKLFLDLHDSIMPYLRRIN-STSKAYATRTLLFLNNQNLKPLAI	471	
QY	473	ELSLPHPDGDFGAGSVKVTYPADQGVGSIWOLAKAYAAVNDGSHQLISHLNTHAAIE	532	
Db	472	ELSLPHPDGDFGAGSVYVTPALGVESSIWLAKAYIVNDSYHQLVSHWLNTHAAVVE	531	
QY	533	PFVIATNRQLSALHPYIKLLHPHFRETMINALARQLINGGGLLELTVPAPKYSMEMSA	592	
Db	532	PFVIATNRHLSCLHPYIKLLYPHYRDTMINSLARLSLVNDGGIIEKTLPLWGRYSMEMSS	591	
QY	593	VYVKDWVFEQALPTDLIKRGVAVEDSSPLGIRLLIQDYPVAVDGLKTIWASKSVWTEY	652	
Db	592	KVYKNWVFTEQALPADLIRKGMAIEDPSPFCGVKLVVEDYPVAVDGLIWAIIKTVWQDY	651	
QY	653	CNYYKSSDDAVQDTELOAWKELREEGHGDKKDEPWPVKMTVQELIDISCTIHWASA	712	
Db	652	VSLYVTSDEKLQDSLOAWKELVEVGRGDKKNEPWPVKMTREDLIEVCISVIWITASA	711	
QY	713	LHAAVNFQGVYVAGYLPNRPPTLSRNPMPGSPGYEELKTNPDKVPKLTITPOLQTLGI	772	
Db	712	LHAAVNFQGVYVAGYLPNRPPTLSRNPMPGSAEELVKSQKAYLKTITTFKQTLIDL	771	
QY	773	SLTEILSRHSSDTLYLGQRESPEWTKDQEPFLSAFAFGKGLSDIEDQIMQMNVDEKWKNR	832	
Db	772	SVTEILSRHASDELVLGERDNPNTSDKEALEAFKKFGNKLAEIEKKLTQRNDEKLRNR	831	
QY	833	SGGVKVPYVTLTPPTBEGGTLTGKIPNSVGI	862	

Db 412 FSTLDEAIQKFLLEHDDTIIPYLRNLN-STSKAYASRTILFLKSDGTLPKLAIELS 470
Qy 476 LPHPDGQFGAVSKYTPADQVSGSIWOLAKAYAAVNDSDGVHQLSHWLNTHAIEBPV 535
Db 471 LPHPDGQFGVSVNYLPAIEGVEATIIWLLAKAYIVNDSCFPHQLSHWLNTHAVVEPV 530
Qy 536 IATNQLSALHIPIYKLLHPHRETWNINARQILINGGGLLELTVPFPAKYSMEASVY 595
Db 531 IATNQLSVLHIPIYKLLHPHYDRTWNINARQISLVNADGIIETFLWGGYAMEISSKY 590
Qy 596 KDWVPEQALPTDLIKRGVAVEDSSPIGIRLLIODYPVANDGLKIWSAISKSWVTEYCN 655
Db 591 KDWVFTDQALPADLIRKGIADVSDTSFHLRLVIEDYPYAVDGLDIWDAIKTWQDYVSI 650
Qy 656 YKSDDAVQKOTELQAWKELREEGDKDPKWPVKQVQVQVQVQVQVQVQVQVQVQV 715
Db 651 YITIDDKIQDSELSQWKEVVEVGHGDKKGPWPKLQTRDGLIHVSSIIWASALHA 710
Qy 716 AVNFQYQYAGYLPNRPILSRNFMPEPGSPYEELKTNPKDFVFLKTIITPQLOTLLGISLI 775
Db 711 AVNFQYQYGGFILNRPILSRRLMEKGTTEVDELATNPQKAYLKIITPQLOTLLDLSVI 770
Qy 776 EILSRHSSTLYLQRESPE-WTKDQEPISAFARFGKLSLSDIEDQIMQVNDKWKNSRG 834
Db 771 EILSRHASDEYVLGQDSAEYVTSOTNALAAPKFGKTLAEIEGQLILRNNSLNRNVG 830
Qy 835 PVKPYTLLFTPSSEGLTKGIPNSVSI 862
Db 831 FVSMPTLLYPSSEGLTFRGIPNSISI 858

RESULT 14
DASYL1
lipoxigenase (EC 1.13.11.12) 2 - soybean
N:Alternate names: carotene oxidase 2; lipoxidase 2
C:Species: Glycine max (soybean)
C:Date: 31-Mar-1989 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: A28161; A30831; A37160; S13536
R:Shibata, D.; Steczko, J.; Dixon, J.E.; Andrews, P.C.; Hermodson, M.; Axelrod, B.
J. Biol. Chem. 263, 6816-6821, 1988
A:Title: Primary structure of soybean lipoxigenase L-2.
A:Reference number: A28161; MUID:88198254; PMID:2834391
A:Accession: A28161
A:Molecule type: mRNA
A:Residues: 1-865 <SH2>
A:Cross-references: UNIPROT:P09439; GB:J03211; NID:gl70013; PIDN:AAA33987.1; PID:gl70014
A:Note: There are no disulfide bonds
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.
Plant Mol. Biol. 7, 11-23, 1986
A:Title: Two soybean seed lipoxigenase nulls accumulate reduced levels of lipoxigenase
A:Reference number: A30831
A:Accession: A30831
A:Molecule type: mRNA
A:Residues: 232-262, 'NL', 265-312, 'Y', 314-362, 'E', 364-399, 'P', 401-427, 'H', 429-485, 'G', 487
A:Cross-references: GB:M16876
A:Experimental source: clone pLX-65
A:Note: due to a frameshift error, residues in the region 691-865 do not correspond to
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.
unpublished results, cited by Yenofsky, R.L., Fine, M., and Liu, C., in Mol. Gen. Genet.
A:Reference number: A37160
A:Accession: A37160
A:Molecule type: mRNA
A:Residues: 232-262, 'NL', 265-312, 'Y', 314-399, 'PK', 402-427, 'H', 429-485, 'G', 487-501, 'G', 501
A:Note: this is a revision to the sequence from reference A30831
R:Shibata, D.; Kato, T.; Tanaka, K.
Plant Mol. Biol. 16, 353-359, 1991
A:Title: Nucleotide sequences of a soybean lipoxigenase gene and the short intergenic re
A:Reference number: S13381; MUID:91370880; PMID:1909908
A:Accession: S13536
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 859-865 <SH2>
A:Cross-references: ENML:X56139; NID:gl8745; PIDN:CAA39605.1; PID:g829267
C:Comment: In soybean, four isozymes are found with distinct electrophoretic properties.
C:Function:
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis pent
C:Superfamily: lipoxigenase
C:Keywords: fatty acid oxidation; iron; metalloprotein; oxidoreductase
P:527,532,718,722,865/Binding site: iron (His, His, Asn, Ile) #status predicted
Query Match 60.6%; Score 2745.5; DB 1; Length 865;
Best Local Similarity 59.6%; Pred. No. 4.le-176;
Matches 526; Conservative 129; Mismatches 190; Indels 37; Gaps 11;
Qy 1 MFLEKIVDAITGDKGKVKGTIVLMKKNVLDL-----TDIN--ASVLD 42
Db 1 MFSVPGVSGILNRGGGHKIGTVLMRKXNLDJFNSVADLTGNVGGILGTGLNVVGSILD 60
Qy 43 GVLEFLGRVRLLELISYVNDPANGLOGKRKAAYLENWLTNSTPIAAGESAFRTFOWD 102
Db 61 NLTAFLGRSVALQLISATK-PLANG-KGKVGKDTFLEGIIVSLPTLGAGESAFNIQFEW- 117
Qy 103 DEBFGVCPAFIINKHSEFELKSLTLEDVNHGKHFVCSWVYPANKYKSDRIFFANQ 162
Db 118 DESMGIPGAFYIKNMQVEFYKSLTLEDVNPQGTIRFVCSWVYNTLYKSVRIFFANH 177
Qy 163 AYLSETPDILRKYRENELVTLRGDGTGKLEMDRVVYAYNDLGDPKGDLRSPVLG 222
Db 178 TVPSETPAALVGYREBELKNLRGDKGERKHRIYDYVDYNDLGNPDHGFARPILG 237
Qy 223 GSSEYPPRRGRTGKPTKDPNSESRIPLMLSDIYVPRDERFHHIKLSDFLTALKSI 282
Db 238 GSSTHPYPRGRTGRTYPRKDNSEK-----PGEVYVPRDENFGLKSSDFLAGIKSL 291
Qy 283 VQLLLPEKALFD--STHNEPDSPELVKVEGKILPQGPILLKAITDSIPLLEIKELLR 340
Db 292 SQYVLPAFESVFDLNFPTNEPDSFQDVRDLHEGGIKLP---TEVISIMPLPVVKELFR 347
Qy 341 SDGGLFKYPPQVTOEDKTAWRTDEEGRMLAGVNPVILSRLOEFPKSLDKPKIYGN 400
Db 348 TDGSOVLKPPPHVQVSKSAMWDEEFARWAGVNPVIRGLOEFPKSLDKPKIYGN 407
Qy 401 QNSTITREQIEDKLDGLTIDEAKTNRLFIINHHDIILMPYLRRINTSDTKYASRTLLF 460
Db 408 QTSKITADALD--LDGYTVDEALSRRLFMDLDYHDFVMPYIRRN-QTYAKAYATRTILF 464
Qy 461 LDNGTILKPSAIELSLPHPDGQFGAVSKVTPADQVSGSIWOLAKAYAAVNDSDGVHQL 520
Db 465 LRENGTLKPAVIAELSLPHPDGDLGSAVSQVILPAKEGVESTIWLIAKAYVNVVNDSCYHQL 524
Qy 521 ISHWLNTHAATEPVIATNRQLSALHPYKLLHPHRETWNINARQILINGGGLLELT 580
Db 525 MSHWLNTHATEPVIATNRHLSALHPYKLLTTPHYRDTMNINARQSLNADGIIERS 584
Qy 581 VFPKYSMEASVAVYKDWVPEQALPTDLIKRGVAVEDSSSPILGIRLLIODYPVAVDGLK 640
Db 585 FLPSKHSVMSAVYKDWVFTDQALPADLIRKGIADVSDTSFHLRLVIEDYPYAVDGL 644
Qy 641 IWSAISKSWVTEYCNYYKSDDAVQKOTELQAWKELREEGDKKDEPWPVPMQVQBELI 700
Db 645 IWSAIAIKTWQVQVSVLYIYARDDVDPDSELOQWKEAVEKGHGLDKDKPWPVKLQITIELV 704
Qy 701 DSCITTIWIASALHAANFGQYVAGVLPNRPILSRNFMPEPGSPYEELKTNPKDFVPLK 760
Db 705 EICITIIWIASALHAANFGQYVAGVLPNRPILSRNFMPEPGSPYEELKTNPKDFVPLK 764
Qy 761 TITPOLQTLGILSILSILSRHSSTLYLQRESPEWTKDQEPISAFARFGKLSLSDIEDQI 820
Db 765 TITSKFTQTLVDLSVIELSRHASDEVVLGQDNPHWTSDSKALQAFQKFGNKLXIEEKL 824
Qy 821 MQMNVDEKWKNSRGPKVYPTLLFTPSSEGLTKGIPNSVSI 862
Db 825 ARKNNDQSLNRLGVQLPYTLLHPNSE-GLTCRGIPNSISI 865

RESULT 15

S07075
 lipoxigenase (EC 1.13.11.12) 2 [similarity] - garden pea
 C:Species: Pisum sativum (garden pea)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: S07075
 R:Ealing, P.M.; Casey, R.
 Biochem. J. 264, 329-332, 1989
 A:Title: The cDNA cloning of a pea (Pisum sativum) seed lipoxygenase. Sequence comparison
 A:Reference number: S07075; MUID:90147555; PMID:2515855
 A:Accession: S07075
 A:Molecule type: mRNA
 A:Residues: 1-864 <EAL>
 A:Cross-references: UNIPROT:P14856; EMBL:X17061; NID:g20801; PIDN:CAA34906.1; PID:g20802
 C:Superfamily: lipoxygenase
 C:Keywords: oxidoreductase

Query Match	60.2%	Score 2731.5;	DB 1;	Length 864;
Best Local Similarity	60.1%	Pred. No. 3.6e-175;		
Matches 526;	Conservative 129;	Mismatches 183;	Indels 37;	Gaps 11;
Qy	10	ITG-KDDGKKYKGVVLMKKNVLDFT-----DINASVLDGVLEFLGR	50	
Db	5	VTGLNKGHKIRGTWLMKKNVLDFTIVSIGGNVHGVIDSGINIIGSTLDGLTAFLGR	64	
Qy	51	RVSLELISSVNADPANGLOGKRSKAAVLEWLTNSTPIAGESAFTVFDWDEEFGVPG	110	
Db	65	SVSLQLISATKSD-ANG-KGKVGKDTFLEGVLASLPTLGAGESAFNIHFEN-DHEMGIPG	121	
Qy	111	AFITIKNLHFSEFFLKSLTLEDVPHNKHVFCNWSWYVANKYKSDRIFFFANQAVLPSETP	170	
Db	122	AFYIKNVMQVEFFLKSLTLEDVPHNKHVFCNWSWYVANKYKSDRIFFFANQAVLPSETP	181	
Qy	171	DTLRKYRENEVLTRGCGTGKLEEDRWYDYAYNLDGDPKQDLSRPVLGSSSEYYP	230	
Db	182	SPLVKYREELQTLRGDGTGRKLERHYDYVYNDLGNPDHGEHLARPILGSSSTHPYP	241	
Qy	231	RGRTGRPTKTDNSESRIPLMSLDIYVPRDERFGHILKSDFTFALKSIIVQLLPEF	290	
Db	242	RGRTGRPTKTDNSEK-----PATETVYPRDENFGLKSSDFLAYGIKSVQCVVPAP	296	
Qy	291	KALFD--STHNEFSFEDVLKLYEGGKLPQGLIKAITDSIPLEILKELLRSDEGEGLFK	348	
Db	297	ESAFDLNFTNFEFSFQDVRNLFEGGKLP----LDVISTLSPLPVKEIFRTDGEQVLK	352	
Qy	349	YPTPQVIOEDKTAMRTDEFGREMLAGVNPVVISRLQEPFKSLDPKIYQNQNSTIRE	408	
Db	353	FTPPHIVIRVSKSAWMTDEFAREMLAGVNPVPCWIRGLQEPFKSLDPKIYQNQNSTIRE	412	
Qy	409	QIEDKLDGLTIDEALKTNRLFILNHHDLMPYLRINTSTDTKYASRTLLFLQDNGTLK	468	
Db	413	VL--NLDGCTIDEALASGRFLDYHDTFIPFLRRIN-ETSAKAYATRTILFLKENGTLK	469	
Qy	469	PSATELSLPHDPDQGFAGSVYVTPADQGVGSIWOLAKAYAVNDSGVHOLISHWLNT	528	
Db	470	PVALIELSLPHDPDGKSGFVSVILPADEGVESTIWLAKAYVVDNSCYHQLMSHLNTH	529	
Qy	529	AAIEFPVIATNRQLSALPIYKLLHPHRET-MNINALARQILNGGGLLETVFPKYS	587	
Db	530	AVIEFPVIATNRQLSVHPINKLLAPHYVDTMNNINALARDSLINANGLIERSFLPSKYA	589	
Qy	588	MEMSAVYKDWVFPQALPTDLIKRGVAVESSPLGRILLIODYPYAVDGLKIWSAISK	647	
Db	590	VEMSSAVYKVVFTDQALPNDLKENMAVKOSSPYGLRLIEDYPYAVDGLLEIWTAKT	649	
Qy	648	WTEYCNYYKSDDAVQKDTLQAWKELREBHGDKKDEPWWPKMOTVQELIDSCITTI	707	
Db	650	WQDVSYLYATDNDIKNDSELOHWWKEVVEKGHGDLDKPKWPKLQTFDELVEVCTIII	709	
Qy	708	WTASALHAAVNFGQVYAGYLPNRPITLGRNFMPEPGSPYEELKTNPDKVLKITTPOLQ	767	
Db	710	WTASALHAAVNFGQVYAGYLPNRPITLGRNFMPEPGSPYEELKTNPDKVLKITTPKRFQ	769	

Qy	768	TLIGISLIELSRHSSTLYLGQRESPETKDOEPLSAPARFGKLSIEDIQIMQNVDE	827	
Db	770	TLIDLSVIELSRHSASDEVYLGQREPHWTSDSKALQAFQFGNKLAEIAEAKLTNNNDP	829	
Qy	828	KWKNRSGPVKVPYTLTLPFTSEGGLTCKGIPNSVSI	862	
Db	830	SLYHRVGPVQLPYTLTLPSSKEGLTFRGIPNSISI	864	

Search completed: March 10, 2005, 19:02:52
 Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 10, 2005, 18:40:16 ; Search time 178 seconds
(without alignments)
2479.844 Million cell updates/sec

Title: US-10-731-642A-1
Perfect score: 4534
Sequence: 1 MFLEKIVDAITGKDDGKKV.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4534	100.0	862	Q43800	Q43800 nicotiana t
2	4095	90.3	862	Q9FT17	Q9FT17 lycopersico
3	3934	86.8	862	Q43191	Q43191 solanum tub
4	3819.5	84.2	861	Q6X5R8	Q6X5R8 nicotiana a
5	3816.5	84.2	861	Q6X5R7	Q6X5R7 nicotiana a
6	3695	81.5	857	Q41238	Q41238 solanum tub
7	3693	81.5	860	Q43190	Q43190 solanum tub
8	3688	81.3	860	LOXA_LYCES	P38415 lycopersico
9	3643.5	80.4	861	Q24379	Q24379 solanum tub
10	3641.5	80.3	861	Q98C16	Q98C16 solanum tub
11	3634.5	80.2	861	Q22508	Q22508 solanum tub
12	3633.5	80.1	864	Q49150	Q49150 solanum tub
13	3632.5	80.1	864	LOX1_SOLATU	P37831 solanum tub
14	3625.5	80.0	859	Q24273	Q24273 lycopersico
15	3625.5	80.0	861	Q43189	Q43189 solanum tub
16	3624.5	79.9	859	LOXB_LYCES	P38416 lycopersico
17	3622.5	79.9	861	Q22507	Q22507 solanum tub
18	3603.5	79.5	844	Q9SAP1	Q9SAP1 solanum tub
19	3550	78.3	873	Q93YI8	Q93YI8 corylus ave
20	3455.5	76.2	862	Q9LEA9	Q9LEA9 prunus dulc
21	3424.5	75.5	862	Q8W4X6	Q8W4X6 prunus dulc
22	3403	75.1	865	Q93WZ2	Q93WZ2 goseypium h
23	3288.5	72.5	884	Q7X9G5	Q7X9G5 fragaria an
24	3228	71.2	857	Q8GV02	Q8GV02 brassica na
25	3202.5	70.6	859	LOX1_ARATH	Q65327 arabidopsis
26	3137.5	69.2	876	Q41430	Q41430 solanum tub
27	3106	68.5	881	Q9M463	Q9M463 cucumis sat
28	3066.5	67.6	697	Q24377	Q24377 solanum tub
29	3054	67.4	854	Q9FNX7	Q9FNX7 arabidopsis
30	3037	67.0	882	Q9LUW0	Q9LUW0 arabidopsis
31	3003.5	66.2	858	Q9ZU05	Q9ZU05 persea amer

32	2914	64.3	878	2	Q42704	Q42704 cucumis sat
33	2911	64.2	878	2	Q42710	Q42710 cucumis sat
34	2894	63.8	857	1	LOX3_SOYEN	P09186 glycine max
35	2872	63.3	877	2	Q42705	Q42705 cucumis sat
36	2837	62.6	861	1	LOX3_PEA	P09918 pisum sativ
37	2793.5	61.6	877	2	Q8S6D6	Q8S6D6 oryza sativ
38	2789.5	61.5	865	2	Q24320	Q24320 phaseolus v
39	2782.5	61.4	864	2	Q8W0V2	Q8W0V2 zea mays
40	2779.5	61.3	864	2	Q9AXG8	Q9AXG8 zea mays
41	2777	61.2	858	2	Q04919	Q04919 vicia faba
42	2746	60.6	866	2	Q39870	Q39870 glycine max
43	2745.5	60.6	865	1	LOX2_SOYBN	P09439 glycine max
44	2731.5	60.2	864	1	LOX2_PEA	P14856 pisum sativ
45	2730.5	60.2	866	2	Q8S6D9	Q8S6D9 oryza sativ

ALIGNMENTS

RESULT 1
Q43800 PRELIMINARY; PRT; 862 AA.
ID Q43800
AC Q43800;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN Name=Lox1;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cell suspension;
RA Veronesi C., Fournier J., Rickauer M., Marolda M.,
RA Esquerre-Tugaye M.T.;
RT "Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA (PCR95-009).";
RL Plant Physiol. 108:1342-1342(1995).
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; X84040; CAA58859.1; -;
DR PIR; S57964; S57964.
DR HSSP; P08170; IFGT.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR001246; Plant lipoxynase.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTLPXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Dioxigenase; Oxidoreductase.
SQ SEQUENCE 862 AA; 97552 MW; D2E7B8D323D5CE34 CRC64;
Query Match 100.0%; Score 4534; DB 2; Length 862;


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Best Local Similarity 100.0%; Pred. No. 1.1e-293;
Matches 862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFLEKIVDAITGKDDGKKVGTVMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISV 60
Db 1 MFLEKIVDAITGKDDGKKVGTVMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISV 60
Qy 61 NADPANGLOGKRSKAAYLENLMTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFS 120
Db 61 NADPANGLOGKRSKAAYLENLMTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFS 120
Qy 121 EFFLKSITLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSTPTDLKRYENE 180
Db 121 EFFLKSITLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSTPTDLKRYENE 180
Qy 181 LVTLRGDTGKLEWDRVYDVAAYNDLGDPPKQDLSRPVLGGSEYPPRRGRTGRKPT 240
Db 181 LVTLRGDTGKLEWDRVYDVAAYNDLGDPPKQDLSRPVLGGSEYPPRRGRTGRKPT 240
Qy 241 KTDPNSESRIPLMSLDIYVPRDRFPGHILKSDFTFALKSIIVOLLPEFKALFDSTHNE 300
Db 241 KTDPNSESRIPLMSLDIYVPRDRFPGHILKSDFTFALKSIIVOLLPEFKALFDSTHNE 300
Qy 301 FDSFEDVLKYEYGGIKLPQGPLLKAITDSIPIELIKELLRSDDGGLFKYPTPQVIQEDKT 360
Db 301 FDSFEDVLKYEYGGIKLPQGPLLKAITDSIPIELIKELLRSDDGGLFKYPTPQVIQEDKT 360
Qy 361 AWRDDEFGREMLAGVNPVIISRLQEPFPPKLDPKIYGNQNSTITREQIEDKLDGLTID 420
Db 361 AWRDDEFGREMLAGVNPVIISRLQEPFPPKLDPKIYGNQNSTITREQIEDKLDGLTID 420
Qy 421 EAIKTNRLFLINHHDILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHD 480
Db 421 EAIKTNRLFLINHHDILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHD 480
Qy 481 GDQFGAVSKVYTPADQGVGSGIWLAKAYAAVNDGSGVHQLISHMLNTHAAIEPFVIATNR 540
Db 481 GDQFGAVSKVYTPADQGVGSGIWLAKAYAAVNDGSGVHQLISHMLNTHAAIEPFVIATNR 540
Qy 541 QLSALHPIYKLLHPHFRMTMINALARQLINGGGLLELTVFPAPKYSMEMSAVVYKQWVF 600
Db 541 QLSALHPIYKLLHPHFRMTMINALARQLINGGGLLELTVFPAPKYSMEMSAVVYKQWVF 600
Qy 601 PEQALPTDLIKRGVAVDESSPLGRLIIOYPAVDGLKWSATKSWTEVCNYYKSD 660
Db 601 PEQALPTDLIKRGVAVDESSPLGRLIIOYPAVDGLKWSATKSWTEVCNYYKSD 660
Qy 661 DAVQKDTLQAWKELREEGHDKKDEPWPMPQVTVQBLIDSCITTIWIASALHAANVFG 720
Db 661 DAVQKDTLQAWKELREEGHDKKDEPWPMPQVTVQBLIDSCITTIWIASALHAANVFG 720
Qy 721 QYPYAGYLPNRPPTLSRNPMPGSPYBELKTNPKVFLKTIITPOLQLLGISLIEILSR 780
Db 721 QYPYAGYLPNRPPTLSRNPMPGSPYBELKTNPKVFLKTIITPOLQLLGISLIEILSR 780
Qy 781 HSSDTLYLGQRESPEWTQDPLSAFAFGKLSIDIEQIMQMVDEKWKNSGPKVPY 840
Db 781 HSSDTLYLGQRESPEWTQDPLSAFAFGKLSIDIEQIMQMVDEKWKNSGPKVPY 840
Qy 841 TLLPPTSEGLTGKIPNSVSI 862
Db 841 TLLPPTSEGLTGKIPNSVSI 862

RESULT 2
Q9FT17 ID Q9FT17 PRELIMINARY; PRT; 862 AA.
AC Q9FT17:
DT 01-MAR-2001 (TreeBLrel. 16, Created)
DT 01-MAR-2001 (TreeBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TreeBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
QS Lycopersicon esculentum (Tomato).
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Pan Z., Feng Q., Gilchrist D.G., Bostock R.M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Lipoate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC EMBL; AY008278; AAG21691.1; -.
DR HSSP; P08170; 1F8N
DR GO; GO:000506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR001246; Plant_lipoxygenase.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
DR DIOXYGENASE; Oxidoreductase.
SQ SEQUENCE 862 AA; 97504 MW; F2E03A209C8B7714 CRC64;

Query Match 90.3%; Score 4095; DB 2; Length 862;
Best Local Similarity 88.3%; Pred. No. 2.2e-264;
Matches 762; Conservative 55; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MFLEKIVDAITGKDDGKKVGTVMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISV 60
Db 1 MILNKIVDSITGKDDGKKVGTVMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISV 59
Qy 61 NADPANGLOGKRSKAAYLENLMTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFS 120
Db 61 NADPANGLOGKRSKAAYLENLMTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFS 119
Qy 121 EFFLKSITLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSTPTDLKRYENE 180
Db 121 EFFLKSITLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSTPTDLKRYENE 179
Qy 181 LVTLRGDTGKLEWDRVYDVAAYNDLGDPPKQDLSRPVLGGSEYPPRRGRTGRKPT 240
Db 181 LVTLRGDTGKLEWDRVYDVAAYNDLGDPPKQDLSRPVLGGSEYPPRRGRTGRKPT 239
Qy 241 KTDPNSESRIPLMSLDIYVPRDRFPGHILKSDFTFALKSIIVOLLPEFKALFDSTHNE 300
Db 241 KTDPNSESRIPLMSLDIYVPRDRFPGHILKSDFTFALKSIIVOLLPEFKALFDSTHNE 299
Qy 301 FDSFEDVLKYEYGGIKLPQGPLLKAITDSIPIELIKELLRSDDGGLFKYPTPQVIQEDKT 360
Db 301 FDSFEDVLKYEYGGIKLPQGPLLKAITDSIPIELIKELLRSDDGGLFKYPTPQVIQEDKT 359
Qy 361 AWRDDEFGREMLAGVNPVIISRLQEPFPPKLDPKIYGNQNSTITREQIEDKLDGLTID 420
Db 361 AWRDDEFGREMLAGVNPVIISRLQEPFPPKLDPKIYGNQNSTITREQIEDKLDGLTID 419
Qy 421 EAIKTNRLFLINHHDILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHD 480
Db 421 EAIKTNRLFLINHHDILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHD 480
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Db 420 EAVKTNRLFILNHHDIIMPVRRINTTTNTKMYATRTLLFLODGTGLKPLAIELSLPHD 479
Qy 481 GQOFGAVSVYTPADQGVGSIWQAKAAVANDSGVHOLISHWLNTHAAIEPFVIATNR 540
Db 480 GQOFGAVSEVTFSDQGVGSIWQAKAAVANDSGVHOLISHWLNTHVTFVFIATNR 539
Qy 541 QLSALHPYIKLHPHFRMTNINARQILINGGGLLELTFPPAKYSMEMSAVVYKDWYF 600
Db 540 QLSVLHPHKLHPHFRMTNINARQILINGGGLLELTFPPAKYSMEMSSVYKDWIF 599
Qy 601 PEQALPTDLIKRGVAVEDSSPLGTRILLIOTDYPYAVDGLKIWSAISKSWTEYCNYYKSD 660
Db 600 PEQALPADLIKRGVAVEDSSPHGVRLLIQDYPYAVDGLKIWSAISKSWTEYCNYYKSD 659
Qy 661 DAVQKDTELQAWKRELREBGHGDKDEPWPMPKMTVOELIDSTTIWIASALHAANFG 720
Db 660 DAVQDAELQAWKRELREBGHGDKDEPWPMPKMSVQELIDSTTIWIASALHAANFG 719
Qy 721 QYPYAGYLPNRPRTLNRNFMPEGSPSEYEELKTNPKVFLKTTIPQLQTLGLISLIELSR 780
Db 720 QYPYAGYLPNRPRTLNRKFMPEGSAEYELKRNPDNPNVFLKTTIPQLQTLGLISLIELSR 779
Qy 781 HSDTYLILGQDSPEWTKDQELSAFARFGKLSLIEDOIMQNVDP-EKWKRSRGPVKVP 839
Db 780 HASDLYLIGQDSPEWTKDQELSAFARFGKLSLIEDRIIQMNGDNQKWKRSRGPVKVP 839
Qy 840 YTLFPTSEGLTGKIPNSVSI 862
Db 840 YTLFPTSEGLTGKIPNSVSI 862

RESULT 3
Q43191 PRELIMINARY; PRT; 862 AA.
AC Q43191;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
CN Name=POTLX-3;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolomiets M.V., Hannapel D.J., Gladon R.J.;
RT "Nucleotide Sequence of a cDNA Clone for a Lipoxigenase from Abscisic
RT Acid-Treated Potato Leaves (Accession No. U60202) (PGR96-069).";
RL Plant Physiol. 112:446-446 (1996).
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; U60202; AAB67865.1; -.
DR PIR; T0775; T0775.
DR HSSP; P08170; 1FGT.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPRO00907; Lipoxigenase.
DR InterPro; IPRO01024; Lipoxigenase.
DR InterPro; IPRO01246; Plant_lipoxigenase.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.

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DR PRINTS; PRO0087; LIPOXYGENASE.
DR PRINTS; PRO0468; PLTLPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Dioxigenase, Oxidoreductase.
SQ SEQUENCE 862 AA; 97777 MW; 94667A9F56041E89 CRC64;

Query Match      86.8%; Score 3934; DB 2; Length 862;
Best Local Similarity 85.1%; Pred. No. 1.2e-253;
Matches 735; Conservative 64; Mismatches 61; Indels 4; Gaps 3;

Qy 1 MFELKIVDAITGK--DDGKKVGTIVLMKKNVLDFTDINASVLDGVLEFLGRVSLSELIS 58
Db 1 MLEKIVFAISGRSEDNGKKVGTIVLMKKNVLDNFVNASLIDGVLEFLGRVSLSELIS 60
Qy 59 SYNADPANGLOGKRSKAAAYLENWLTNSTPIAAGESAFRVTPDWDDEEFGVPGAFIKNLH 118
Db 61 VVHADPGNSLOGKRSNPAYLEKWLTTGTSLVAGESAFDVTDPW-DEDIGVPGAFIINNPH 119
Qy 119 RSEFLKSLTLEDVPHGKVFHVCNSWYYPANKYSDRIFFANQAYLPSSETDPTLRKYRE 178
Db 120 FNEFYKSLTLEDVPHGKVFHVCNSWYYPANKYKSERIFFANQAYLPGETPEPLRNYRE 179
Qy 179 NELVTRGDGTGKLEWRDVRVYDYAYNDLGDGDKDLSRPVLGGSSEYPPRRGRTRGK 238
Db 180 KELVNLRGNGKLEWRDVRVYDYALYNDLGDPEKQKQVARTILGGSSEYPPRRGRTRGK 239
Qy 239 PTKTDPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFALKSIYQLLPEFKALFDSTH 298
Db 240 PTKADPKSESRIPLMLSLDIYVPRDERFGHIKLSDFLTVALKSIYQFLPEFQALFDSTP 299
Qy 299 NEFDSFEDVLKLYEGGIKLPQGPLKAITDSIPLILKELRSDEGLFKYFTPTQVIOED 358
Db 300 DEFDSFEDVLKLYEGGIKLPQGPLKALTDSIPLILKELRIINTDEGKFKFTPTQVIOED 359
Qy 359 KTAWRTDEEFGREMLAGVNPVIISRLQFPFKSKLDPKYGNONSTITREQIEDKLDGJT 418
Db 360 KSSWRTDEEFAREMLAGVNPVIISRLQFPFKSKLDSEVYGNONSTITKEHENTLDGJT 419
Qy 419 IDEAIKTNRLFILNHHDIIMPYLRINTSDTKTYASRTLLFLODGTGLKPSAIELSLPH 478
Db 420 IDDAIKTNRLFILNHHDIIMPYVRINT-TNTKLYASRTLLFLODGTGLKPSAIELSLPH 478
Qy 479 PDGDFGAVSVYTPADQGVGSIWQAKAAVANDSGVHOLISHWLNTHAAIEPFVIAT 538
Db 479 PDGDELGAVSVYTPADQGVGSIWQAKAAVANDSGVHOLISHWLNTHAAIEPFVIAT 538
Qy 539 NRQLSALHPYIKLHPHFRMTNINARQILINGGGLLELTFPPAKYSMEMSAVVYKDW 598
Db 539 NRQLSVLHPHKLHPHFRMTNINARQILINAGGVLEMTVFPKAYMEMSAVVYKSW 598
Qy 599 VFPEQALPTDLIKRGVAVEDSSPLGIRLLIOTDYPYAVDGLKIWSAISKSWTEYCNYYK 658
Db 599 VFPEQALPADLIKRGVAVEDSSPHGVRLLIQDYPYAVDGLKIWSAISKSWTEYCNYYK 658
Qy 659 SDDAVQKOTELQAWKRELREBGHGDKDEPWPMPKMTVOELIDSTTIWIASALHAAN 718
Db 659 SDELVLKDNELQAWKRELREBGHGDKDEPWPMPKMTVOELIDSTTIWIASALHAAN 718
Qy 719 FGQYPYAGYLPNRPRTLNRNFMPEGSPSEYEELKTNPKVFLKTTIPQLQTLGLISLIEL 778
Db 719 FGQYPYAGYLPNRPRTLNRNFMPEGSPSEYEELKTNPKVFLKTTIPQLQTLGLISLIEL 778
Qy 779 SRHSDDTYLIGQDSPEWTKDQELSAFARFGKLSLIEDOIMQNVDP-EKWKRSRGPVKV 838
Db 779 SRHASDEIYLIGQDSSEWTKDQELSAFERFGKLSLIEDOIIQWNGDKKWKRSRGPVNV 838
Qy 839 PYTLFPTSEGLTGKIPNSVSI 862
Db 839 PYTLFPTSEGLTGKIPNSVSI 862

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RESULT 4
Q6X5R8 PRELIMINARY; PRT; 861 AA.
AC Q6X5R8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Lipoxigenase.
GN Name=Loxib;
OS Nicotiana attenuata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=49451;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RX PubMed=14675445;
RA Halitschke R., Baldwin I.T.;
RT "Antisense LOX expression increases herbivore performance by
RT decreasing defense responses and inhibiting growth-related
RT transcriptional reorganization in Nicotiana attenuata.";
RL Plant J. 36:794-807(2003).
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- SIMILARITY: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; AY254346; AAP83135.1; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR001246; Plant lipoxynase.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTLPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Dioxigenase; Oxidoreductase.
SQ SEQUENCE 861 AA; 97246 MW; AF28A25ADA710E21 CRC64;

Query Match 84.2%; Score 3819.5; DB 2; Length 861;
Best Local Similarity 81.8%; Pred. No. 5,4e-246;
Matches 706; Conservative 80; Mismatches 74; Indels 3; Gaps 3;

Qy 1 MF-LEKIVDAITGDKDKKVGTVVLMKKNVLDFTDINASVLDGVLEPLGRVSLLEISS 59
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MFPIKNIVDGLGHNSDKKVGIVVMKKNALDFTDIAGSVVDGVLEFVGQKVSILQLISS 60
Qy 60 VNAPANGLOKRSKAAVLENLNTNSTPIAGESAFRTVDDEEFCVPGAFIKNLHF 119
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 AHGPDANDLOQKHSNLALENWLITITITLPTAGESAIGVTFTDW-DEEFLPGAFIKNLHF 119
Qy 120 SEFFLKSITLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPTLTKYREN 179
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 TEFLKSVTLEDVPHNGVHVCNSWVYPANKYKSDRIFFANKYLPSETPAPLLKYREN 179
Qy 180 ELVTLRGSGTGKLEBWDVYDAYVNDLGDPPKQDLSRPVLGGSSSEYPPRRGRTGRK 239
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
180 ELLTLRGDGTGKLEANDRVYDLYNDLGDPPQGAQHVRLILGGSSDYPPRRGRTGRAP 239
```

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Qy 240 TKTDPNSESRIPLIMSLDIYVPRDEREGHIKLSDFLTALKSIYQLLLPEKALFDSTHN 299
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
240 TRDTPESERIPLLSLDIYVPRDEREGHIKLSDFLTALKSMVQFILPELHALFDSTFN 299
Qy 300 EFDSEFDVLKLYEGGIKLPQGPLLKAITDSIPLEILKELLRSDEGEGFLPKYPTPOVEDK 359
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
300 EFDSEFDVLKLYEGGIKLPQGPLFKALISSIPLEMWKELLRTDCEGIMKPTPLVikedK 359
Qy 360 TAWRTDEEFGREMLAGVNPVILSRLOFPFKSLDPKIYGNQNSTITIREQIEDKLDGLTI 419
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
360 TAWRTDEEFGREMLAGVNPVILSRLOFPFKSLDPKIYGNQNSTITITIOHLEDGLTI 419
Qy 420 DEAKTNRLFILNHHDTLMPVLRINTSTDTKYASRTTLFLOQNGTLKPSAIELSLPH 479
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
420 DEAKTNRLFILNHHDTLMPVLRINTT-TKYASRTTLFLOQNGTLKPSAIELSLPH 479
Qy 480 DGQDFGAVSKYVTPADQGVGSGIWLQAKAYAVNDSGVHQLISHWLNTHAIEPFIATN 539
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
479 DGQDFGAVSKYVTPDTEGVGSIWELAKAYAVNDSGVHQLISHWLNTHAIEPFIATN 538
Qy 540 ROLSAHLPIYKLLHPHRETNNINAROLINGGILELTVFPKYSMENSAAVYKDWV 599
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
539 ROLSVLPHIHKLLHPHFRDTNNINARQILINAGGVLESTVFPKYSMENSAAVYKDWV 598
Qy 600 FPEQALPTDLIKRGVAVEDSSPLGIRLLIQDYVAVDGLKINSAIKSWTEYCNYKYS 659
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
599 FPDQALPTDLIKRGVAVEDSSPHGIRLLIQDYVAVDGLKINSAIKSWTEYCNYKYS 658
Qy 660 DDAVQKDTLQAWKELREHGDKDEPWPKNQTVQELIDSCITITITWASALHAAVNF 719
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
659 DDAVQKDTLQAWKELREHGDKDEPWPKNQTVQELIDSCITITITWASALHAAVNF 718
Qy 720 GQPYAGYLPNRPILSNFMPGSPYBELKTNPKVFLKTIITPOLQTLGLISLIELS 779
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
719 GQPYAGYLPNRPILSNFMPGSPYBELKTNPKVFLKTIITPOLQTLGLISLIELS 778
Qy 780 RHSSDTLYLGORESPWTKDQPLSAFAFKKLSIEDIQIMQNVDEKKNRSGPVKVP 839
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
779 RHSSDTLYLGORESPWTKDQPLSAFAFKKLSIEDIQIMQNVDEKKNRSGPVKVP 838
Qy 840 YTLFPTSEGGLTGKIPNSVSI 862
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
839 YTLFPTSEGGLTGKIPNSVSI 861

RESULT 5
Q6X5R7 PRELIMINARY; PRT; 861 AA.
AC Q6X5R7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Lipoxigenase.
GN Name=Loxib; Synonyms=Lox1a;
OS Nicotiana attenuata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=49451;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RX PubMed=14675445;
RA Halitschke R., Baldwin I.T.;
RT "Antisense LOX expression increases herbivore performance by
RT decreasing defense responses and inhibiting growth-related
RT transcriptional reorganization in Nicotiana attenuata.";
RL Plant J. 36:794-807(2003).
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
```

```
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; AY254347; AAF8136.1; -.
DR EMBL; AY254345; AAF8134.1; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR001246; Plant lipoxynase.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
DR DIOXYGENASE; Oxidoreductase.
KW DIOXYGENASE; Oxidoreductase.
SQ SEQUENCE 861 AA; 97214 MW; 50BBE9BD8420D6ED CRC64;

Query Match 84.2%; Score 3816.5; DB 2; Length 861;
Best Local Similarity 81.7%; Pred. No. 8.6e-246;
Matches 705; Conservative 81; Mismatches 74; Indels 3; Gaps 3;

QY 1 MF-LEKIVDAITGKDDGKVKGTGVTVMKKNVLDFTDINASVLDGVLEFLGRRVSLIELISS 59
DB 1 MFPIKNIVDGLIGHNDSKKVGIVVMKKNALDFTDIAGVVDGVLEFVGQKVSILQLISS 60

QY 60 VNADPANGLOGKSKAAYLENWLNTSTPTAAGESAFRTVFDWDEFGVPGAFIKNLHF 119
DB 61 AHGDPANLQGHKSHPAYLENWLNTTITPTAGESAYGVTFDW-DEEFGVPGAFIKNLHF 119

QY 120 SEFFLKSITLEDVPHNKGKVFVCNWSVYPANKYKSDRIFPANOAYLPSTPTDLKRYEN 179
DB 120 TEFFLKSITLEDVPHNKGKVFVCNWSVYPANKYKSDRIFPANOAYLPSTPTDLKRYEN 179

QY 180 ELTVLRGDSGTGLKLEMDRYDYAYNDLGDGDPKQDLSRPVLGSSSEYPPRRGRTGRKP 239
DB 180 ELLTVLRGDSGTGLKLEMDRYDYAYNDLGDGDPQGAQHVRPILGSSSEYPPRRGRTGRAP 239

QY 240 TKTDNPSRSRPLMSLDIYVPRDRFGHILKSDFLTFALKSIQVLLPPEFKALFDSTHN 299
DB 240 TRTDPESESRIPLLSLDIYVPRDRFGHILKSDFLTFALKSMVQFILLFHALFDSTPN 299

QY 300 EFDSPEDVLKLYEGGKLPQGPPLKAITDSIPLKELLRSDDGRLGPKYPTPOVIOEDK 359
DB 300 EFDSPEDVLKLYEGGKLPQGPPLKAITDSIPLKELLRSDDGRLGPKYPTPOVIOEDK 359

QY 360 TAWRTDEBFREMLAGVNPVIRSRLEQPPPKSLDKPIYGNQNSTITREIQDKLDGLTI 419
DB 360 TAWRTDEBFREMLAGVNPVIRSRLEQPPPKSLDKPIYGNQNSTITREIQDKLDGLTI 419

QY 420 DEAKTNELFLNHHDLMPYLRINTSTDTKYASRLLFLQDNGTKPSAIELSLPH 479
DB 420 DEAKTNELFLNHHDLMPYLRINTSTDTKYASRLLFLQDNGTKPSAIELSLPH 479

QY 480 DGDQFGAVKVTTPADQGVGSIWOLAKAYAVNDGSHQLIHLNTHAATEPEVIATN 539
DB 480 DGDQFGAVKVTTPADQGVGSIWOLAKAYAVNDGSHQLIHLNTHAATEPEVIATN 539

QY 499 RQLSALHPYIKLLHPHFRETMINALARQILINGGLLELTVFPKYSNEMSAVYKDWV 599
DB 500 RQLSVLHPYIKLLHPHFRETMINALARQILINGGLLELTVFPKYSNEMSAVYKDWV 599

QY 600 PPEQALPTDLKRGVAVDESSPLGIRLLIQDYPYAVDGLKTSIAKSWVTEYCNYYKS 659
DB 600 PPEQALPTDLKRGVAVDESSPLGIRLLIQDYPYAVDGLKTSIAKSWVTEYCNYYKS 659

QY 599 FPDQALPTDLKRGVAVDESSPLGIRLLIQDYPYAVDGLKTSIAKSWVTEYCNYYKS 659
DB 599 FPDQALPTDLKRGVAVDESSPLGIRLLIQDYPYAVDGLKTSIAKSWVTEYCNYYKS 659

QY 660 DDAVOKDTLOAWKELREEGHGDKKDEPWPMPKMTQVQELSDSTTTIWIASALHAANVF 719
DB 660 DDAVOKDTLOAWKELREEGHGDKKDEPWPMPKMTQVQELSDSTTTIWIASALHAANVF 719

QY 659 DSIILKDELQAWKELREEGHGDKKDEPWPMPKMTQVQELSDSTTTIWIASALHAANVF 718
DB 659 DSIILKDELQAWKELREEGHGDKKDEPWPMPKMTQVQELSDSTTTIWIASALHAANVF 718

QY 720 GOYPYAGYLPNRPPLSRNPMPEPGSPYEEELKTNPKVFLKTTITPQLQTLGLSLIEILS 779
DB 720 GOYPYAGYLPNRPPLSRNPMPEPGSPYEEELKTNPKVFLKTTITPQLQTLGLSLIEILS 779

QY 719 GOYPYAGYLPNRPPLSRNPMPEPGSPYEEELKTNPKVFLKTTITPQLQTLGLSLIEILS 778
DB 719 GOYPYAGYLPNRPPLSRNPMPEPGSPYEEELKTNPKVFLKTTITPQLQTLGLSLIEILS 778

QY 780 RHSSDTLVILGORESPETKDEPLSAFAFGKLSLSDIEDQINQMNVDKWKNSGPKVYP 839
DB 780 RHSSDTLVILGORESPETKDEPLSAFAFGKLSLSDIEDQINQMNVDKWKNSGPKVYP 839

QY 779 RHTSDEIYLQORDSPKTYDEEPLAFAFGKLSLSDIEDQINQMNVDKWKNSGPKVYP 838
DB 779 RHTSDEIYLQORDSPKTYDEEPLAFAFGKLSLSDIEDQINQMNVDKWKNSGPKVYP 838

QY 840 YTLFPTSEGGITGKIPNSVSI 862
DB 839 YTLFPTSEGGITGKIPNSVSI 861

RESULT 6
Q41238 PRELIMINARY; PRT; 857 AA.
AC Q41238;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Linoate:oxigen oxidoreductase (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94302170; PubMed=8029354; DOI=10.1104/pp.105.1.269;
RA Geerts A., Feltkamp D., Rosahl S.;
RT "Expression of lipoxigenase in wounded tubers of Solanum tuberosum L.";
RL Plant Physiol. 105:269-277(1994).
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of diverse aspects of plant physiology including growth and development, pest resistance, and senescence or responses to wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoate + O(2) = (9Z,11E)-(13S)-13-hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; S73865; AAB31252.1; -.
DR HSP; P08170; 1FCT.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR001246; Plant lipoxynase.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW DIOXYGENASE; Oxidoreductase.
FT NON TER 857 857
SQ SEQUENCE 857 AA; 96585 MW; 3785A24E8DBA8DA7 CRC64;

Query Match 81.5%; Score 3695; DB 2; Length 857;
Best Local Similarity 80.0%; Pred. No. 1.1e-237;
Matches 682; Conservative 84; Mismatches 85; Indels 2; Gaps 2;

QY 10 ITGKDDGKVGKVTVMKKNVLDFTDINASVLDGVLEFLGRRVSLIELISSVNNADPANGLO 69
```

Db 7 IGGHDSKKVGVVMMKKNALDFTDLAGSLTDKI FEALGQKVSFQLLSSVQSDPANGLO 66
Qy 70 GKRSKAAYLENLWNTSPITAAAGESAFRTVDWDEEFGVPCAFI IKNLHSEFFLKSITL 129
Db 67 GKHSNPAYLENFLFTLPLAAGETAFGVTFDW-NEEFGVPCAFI IKNTHINEFFLKSITL 125
Qy 130 EDVNHGKVFVNCWVWPANKYKSDRIFFANQAYLPSETPDLTKYRENEELVTLRGDGT 189
Db 126 EDVNHGKVFVNCWVWPANKYKSDRIFFANQAYLPSETPDLTKYRENEELVTLRGDGT 185
Qy 190 GKLEWDRVYDYAYNDLGDGPKQDLSRPFVLSGSSEYPPRRGRTGKPTKTPDPSSES 249
Db 186 GKREAWDRVYDYAYNDLGNPDQEQNVRTLLGSADYPPRRGRTGKPTKTPDPSSES 245
Qy 250 IPLMSLDIYVPRDERFGHIKLSDFLTKSIVQILLPEKALFDSTHNEFDSFEDVLK 309
Db 246 IPLTSLDIYVPRDERFGHLMKSDFLYALKSVIQQILPELHALFDGTPNFDSEFVLR 305
Qy 310 LYEGGIKLPQGLPKAITDSTPLEILKELLSDEGLFKYPTPOVIOEDKTAWTDEEFG 369
Db 306 LYEGGIKLPQGLPKAITDSTPLEILKELLSDEGLFKYPTPOVIOEDKTAWTDEEFG 365
Qy 370 REMLAGVNPVILSRLOEPPPKSKLDPEAYGNQSTITAEHIEDKLDGLTIDEAKTNRLF 429
Db 366 REMLAGVNPVILSRLOEPPPKSKLDPEAYGNQSTITAEHIEDKLDGLTIDEAMNNKLF 425
Qy 430 ILNHHDILMPYLRINTSTDTKTVASTRLLFLQNGTLKPSAIELSLPHPDGDFGAVSK 489
Db 426 ILNHHDILMPYLRINTSTDTKTVASTRLLFLQNGTLKPSAIELSLPHPDGDFGAVSK 484
Qy 490 VYTPADQGVESIQWAKAYAVNDGSHVQLISHWLNTHAIEPVTATNROLSALHPYI 549
Db 485 VYTPADQGVESIQWAKAYAVNDGSHVQLISHWLNTHAIEPVTATNROLSALHPYI 544
Qy 550 KLLPHFRFTWNIARQILNGGLLELVTFPAKYSMEASVYKDWVPEQALPTDL 609
Db 545 KLLPHFRFTWNIARQILNGGLLELVTFPAKYSMEASVYKDWVPEQALPTDL 604
Qy 610 IKGVAVEDSSPGLRILLIODYPVADGLKIWAKSWVTEYCNYYKSDADAVOKTEL 669
Db 605 IKGVAVEDSSPGLRILLIODYPVADGLKIWAKSWVTEYCNYYKSDADAVOKTEL 664
Qy 670 QAWKELREEGHGDGKDPKPMQVQELIDSCITTIWIASALHAAVNFQYVAGYLP 729
Db 665 QAWKELREEGHGDGKDPKPMQVQELIDSCITTIWIASALHAAVNFQYVAGYLP 724
Qy 730 NRPTLSRNFMEPGSPYEELKTNPKVFLKTTIPQLTLLGILSILIELSRHSDTLYLG 789
Db 725 NRPTLSRNFMEPGSPYEELKTNPKVFLKTTIPQLTLLGILSILIELSRHSDTLYLG 784
Qy 790 QRESPEWTKDQEPISAFARFQKLSIDIEDQIMQMNVDKWNKRGVKKVPTLLFPPTSEG 849
Db 785 QRESPEWTKDQEPISAFARFQKLSIDIEDQIMQMNVDKWNKRGVKKVPTLLFPPTSEG 844
Qy 850 GLTKGIPNSVSI 862
Db 845 GLTKGIPNSVSI 857

RESULT 7

Q43190 PRELIMINARY; PRT; 860 AA.
ID Q43190
AC Q43190;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN Name=FOTLX-2;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
QC lamiales; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolomiets M.V., Hannapel D.J., Gladon R.J.;
RT "Potato Lipoxigenase Genes Expressed During the Early Stages of
RT Tubarization (Accession Nos. U60200 and U60201) (PCR96-065).";
RL Plant Physiol. 112:446-446(1996).
CC -1- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -1- CATALYTIC ACTIVITY: Lipoate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -1- COFACTOR: Iron (By similarity).
CC -1- SIMILARITY: Belongs to the lipoxigenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; U60201; AAB67860.1; -;
DR HSP; P08170; 1FGT.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR Dioxigenase; Oxidoreductase.
KW Dioxigenase; Oxidoreductase.
SQ SEQUENCE 860 AA; 96968 MW; 11FD0D769921053E CRC64;

Query Match 81.5%; Score 3693; DB 2; Length 860;

Best Local Similarity 79.8%; Pred. No. 1.5e-237;

Matches 681; Conservative 86; Mismatches 84; Indels 2; Gaps 2;

Qy 10 ITGKDDKKVGVVMMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISSVADPANGLO 69

Db 10 IGGHDSKKVGVVMMKKNALDFTDLAGSLTDKI FEALGQKVSFQLLSSVQSDPANGLO 69

Qy 70 GKRSKAAYLENLWNTSPITAAAGESAFRTVDWDEEFGVPCAFI IKNLHSEFFLKSITL 129

Db 70 GKHSNPAYLENFLFTLPLAAGETAFGVTFDW-NEEFGVPCAFI IKNTHINEFFLKSITL 128

Qy 130 EDVNHGKVFVNCWVWPANKYKSDRIFFANQAYLPSETPDLTKYRENEELVTLRGDGT 189

Db 129 EDVNHGKVFVNCWVWPANKYKSDRIFFANQAYLPSETPDLTKYRENEELVTLRGDGT 188

Qy 190 GKLEWDRVYDYAYNDLGDGPKQDLSRPFVLSGSSEYPPRRGRTGKPTKTPDPSSES 249

Db 189 GKREAWDRVYDYAYNDLGNPDQEQNVRTLLGSADYPPRRGRTGKPTKTPDPSSES 248

Qy 250 IPLMSLDIYVPRDERFGHIKLSDFLTKSIVQILLPEKALFDSTHNEFDSFEDVLK 309

Db 249 IPLTSLDIYVPRDERFGHLMKSDFLYALKSVIQQILPELHALFDGTPNFDSEFVLR 308

Qy 310 LYEGGIKLPQGLPKAITDSTPLEILKELLSDEGLFKYPTPOVIOEDKTAWTDEEFG 369

Db 309 LYEGGIKLPQGLPKAITDSTPLEILKELLSDEGLFKYPTPOVIOEDKTAWTDEEFG 368

Qy 370 REMLAGVNPVILSRLOEPPPKSKLDPEAYGNQSTITAEHIEDKLDGLTIDEAKTNRLF 429

Db 369 REMLAGVNPVILSRLOEPPPKSKLDPEAYGNQSTITAEHIEDKLDGLTIDEAMNNKLF 428

Qy 430 ILNHHDILMPYLRINTSTDTKTVASTRLLFLQNGTLKPSAIELSLPHPDGDFGAVSK 489

Db 429 ILNHHDILMPYLRINTSTDTKTVASTRLLFLQNGTLKPSAIELSLPHPDGDFGAVSK 487

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QY 490 VYTPADQGVESIMQAKAYAAVNDGSHVHQLISHWLNTHAAIEPVIATNRQLSALHPYI 549
Db 488 VYTPSDQGVESIMQAKAYAAVNDGSHVHQLISHWLNTHAVIEPVIATNRQLSVHPIH 547
QY 550 KLLHPHFRETWNINARQILINGGELLEITVFPKAYKMSAVVYKDWVPEQALPTDL 609
Db 548 KLLYPHFRTWNINARQILINAGVLESTVFPKAFEMSAVVYKDWVFPDQALPADL 607
QY 610 IKRGVAVEDSSPLGIRLLIODYPAVDGLKTSWAKSVWTEYCNYYKSDVAVOKDTL 669
Db 608 VARGVAVEDSSPHGVRLLIEDYPAVDGLEISWAKSVWTDYCSFYGSDEEILKONEL 667
QY 670 QAWKELREEGHGDCKDPFMPFMQVQELIDSCITTIWIASALHAANFQGYPYAGYLP 729
Db 668 QAWKELREVGHGDKKNEPMPMETPQELIDSCITTIWIASALHAANFQGYPYAGYLP 727
QY 730 NRPLSRNFMPEPGSPYEELKTNPKVFLKTIITPOLQTLIGISLIEILSRHSSDTLYLG 789
Db 728 NRPTVSRNFMPEPGSPYEELKKNPKDKAFLKTIITQAQLTLLGVSLEILSRHTTDEIYLG 787
QY 790 QRESPWTKDQEPISAFARFGKLSIDIEDQIMQNMVDEKKNRSQVVPVYTLFPPTSEG 849
Db 788 QRESPWTKDQEPISAFARFGKLSIDIEDQIMQNMVDEKKNRSQVVPVYTLFPPTSEG 847
QY 850 GLTGKIPNSVSI 862
Db 848 GLTGKIPNSVSI 860

RESULT 8
LOXA_LYCES STANDARD; PRT; 860 AA.
AC P38415;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipoxigenase A (BC 1.13.11.12).
GN Name=LOX1.1; Synonyms=LOXA;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Caruso; TISSUE=Pericarp;
RX MEDLINE=95062736; PubMed=797514; DOI=10.1104/pp.106.1.109;
RA Ferrie B.J., Beaudoin N., Burkhardt W., Bowsher C.G., Rothstein S.J.;
RT "The cloning of two tomato lipoxigenase genes and their differential
expression during fruit ripening.";
PL Plant Physiol. 106:109-118(1994).
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
diverse aspects of plant physiology including growth and
development, pest resistance, and senescence or responses to
wounding. It catalyzes the hydroperoxidation of lipids, containing
a cis,cis-1,4-pentadiene structure.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Expressed in germinating seeds as well as in
ripening fruit.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.

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CC ----- AAA53184.1; --
DR HSSP; P08170; 1FGT.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR001246; Plant lipoxynase.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00811; LIPOXYGENASE_2; 1.
DR PROSITE; PS0095; PLAT; 1.
KW Dioxygenase; Iron; Multigene family; Oxidoreductase.
FT DOMAIN 29 159
FT METAL 521 521 Iron (By similarity).
FT METAL 526 526 Iron (By similarity).
FT METAL 712 712 Iron (By similarity).
FT METAL 860 860 Iron (By similarity).
SQ SEQUENCE 860 AA; 96764 MW; 43D1091853469426 CRC64;

Query Match 81.3%; Score 3688; DB 1; Length 860;
Best Local Similarity 79.8%; Pred. No. 3.3e-237;
Matches 681; Conservative 86; Mismatches 84; Indels 2; Gaps 2;

QY 10 ITGKDDGKKVGTVMKKNVLDFTDINASVLDGVLEPLGRVSLLELISSVYNADPANGLO 69
Db 10 IGGHDSKKVGTVMKKNALDFTDLAGSLTDKI FEALGOKVSFQLISSVQSDPANGLO 69
QY 70 GKSKAAVLENWLTNSTPIAAGESAFRTVDWDEEFGVPGAFIKNLHSEFFLKSITL 129
Db 70 GKSNPAYLENFLTITPLAAGETAFGVTFW-NEEFGVPGAFIKNWHINEFFLKSITL 128
QY 130 EDVENHGKVFVCNSWVYPANKYKSDRIFFANQYLPSETDPTLRKYRENELVTLRGDGT 189
Db 129 EDVENHGKVFVCNSWVYSPRYKSDRIFFANQYLPSETPELLRKYRENELVTLRGDGT 188
QY 190 GKLEWRVDYAYNDLGDPPKQDLSRPVLGGSSEYPPRRGTGRKPTDPSER 249
Db 189 GKREAWDRIYDYNLDGNPDQGNVTTLGGSADYPPRRGTGRPTTDPKSES 248
QY 250 IPLMSLDIVPRDERFGHKLSDFLTALKSI VQLLLPEPKALFDSNTHNFDGFEDVLK 309
Db 249 IPLSLSDIVPRDERFGHKLMSDFLYALKSI VQFILPELHALFDGTPNDFSEDFVLR 308
QY 310 LYEGGKILPQGLLKAITDSIPLEILKELRSDEGELFKYPTPQVIOEDKTAWRTDEBF 369
Db 309 LYEGGKILPQGLPKALTDAIPLEMIRELLTDCGELRPPTPLVIKDSKTAWRTDEBFA 368
QY 370 REMLAGNPVVISLQSPPKSKLDPKLYGNQNTITREQIEDKLDGLTIDEAINTNRLF 429
Db 369 REMLAGNPVVISLEFPFKSKLDPELYGNQNTITAEHIEGKLDGLTIDEAINSRLF 428
QY 430 ILNHHDILMPVLRINTSTDTKTYSATLLPLQNGTLKPSAIELSLPHPPDQGFVSK 489
Db 429 ILNHHDILPYLRINTT-TKTYASRLLPLQNGSLKPLAIELSLPHPPDQGFVTSK 487
QY 490 VYTPADQGVESIMQAKAYAAVNDGSHVHQLISHWLNTHAAIEPVIATNRQLSALHPYI 549
Db 488 VYTPSDQGVESIMQAKAYAAVNDGSHVHQLISHWLNTHAVIEPVIATNRQLSVHPIH 547
QY 550 KLLHPHFRETWNINARQILINGGELLEITVFPKAYKMSAVVYKDWVPEQALPTDL 609
Db 548 KLLYPHFRTWNINARQILINAGVLESTVFPKAFEMSAVVYKDWVFPDQALPADL 607
QY 610 IKRGVAVEDSSPLGIRLLIODYPAVDGLKTSWAKSVWTEYCNYYKSDVAVOKDTL 669
Db 608 VARGVAVEDSSPHGVRLLIEDYPAVDGLEISWAKSVWTDYCSFYGSDEEILKONEL 667
QY 670 QAWKELREEGHGDCKDPFMPFMQVQELIDSCITTIWIASALHAANFQGYPYAGYLP 729
Db 668 QAWKELREVGHGDKKNEPMPMETPQELIDSCITTIWIASALHAANFQGYPYAGYLP 727
QY 730 NRPLSRNFMPEPGSPYEELKTNPKVFLKTIITPOLQTLIGISLIEILSRHSSDTLYLG 789
Db 728 NRPTVSRNFMPEPGSPYEELKKNPKDKAFLKTIITQAQLTLLGVSLEILSRHTTDEIYLG 787
QY 790 QRESPWTKDQEPISAFARFGKLSIDIEDQIMQNMVDEKKNRSQVVPVYTLFPPTSEG 849
Db 788 QRESPWTKDQEPISAFARFGKLSIDIEDQIMQNMVDEKKNRSQVVPVYTLFPPTSEG 847
QY 850 GLTGKIPNSVSI 862
Db 848 GLTGKIPNSVSI 860
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Db 668 QAWKEVREVGDKGNKPWAEWETPQELIDSCITTIWIASALHAANVFGQYPVAGYLP 727
Qy 730 NRPTLSRNFMPGSPGYEELKTNPKVFLKTIIPOLQTLGSLIELSRHSSDTLYLG 789
Db 728 NRPTVSRKFMPEPGTPEYELKXNPKAFKTKITTAQLQTLGSLIELSRHTTDEIYLG 787
Qy 790 QRESPEWTKDQEPISAFARFGKKISDIEDQIMQMNVDKWNRSRGPVVPYTLFPPTSEG 849
Db 788 QRESPEWTKDQEPISAFARFGKKISDIEDQIMQMNVDKWNRSRGPVVPYTLFPPTSEG 847
Qy 850 GLTGKIPNSVSI 862
Db 848 GLTGKIPNSVSI 860

RESULT 9
ID O24379 PRELIMINARY; PRT; 861 AA.
AC O24379;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_Taxid=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tuber;
RX MEDLINE=96355454; PubMed=8702864; DOI=10.1074/jbc.271.35.21012;
RA ROYO J.N., Vancanneyt G., Persz A.G., Sanz C., Stormann K., Rosahl S.,
Sanchez-Serrano J.J.;
RT "Characterization of three potato lipoxigenases with distinct
RT enzymatic activities and different organ-specific and wound-regulated
RT expression patterns.";
RL J. Biol. Chem. 271:21012-21019 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Tuber;
RA ROYO J.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; X95513; CAA64766.1; -.
DR HSSP; P08170; 1FGT.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR001246; Plant lipoxigenase.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTIPOXYGNASE.
DR SMART; SMO0308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW DiOxygenase; Oxidoreductase.
SQ SEQUENCE 861 AA; 97066 MW; 25783F32C69BFA26 CRC64;

Query Match 80.4%; Score 3643.5; DB 2; Length 861;
Best Local Similarity 79.2%; Pred. No. 3e-234;
Matches 675; Conservative 82; Mismatches 92; Indels 3; Gaps 3;
Qy 12 GKDDGKVKGTIVLMKKNVLDFTDINASVLGVLEFLGRRVSLBELISSVNADPANGLOGK 71
Db 12 GPDSKLLKGTVMNMKNALDFTDLAGSLTDKAFELGQTVSFQLISSVQDPTNGLOGK 71
Qy 72 RSKAAYLENLWNTSTPIAAG-ESAFRTVTFDWDDEFGVPGAFIKNLHFSFEFFLSLTLE 130
Db 72 HSNPAYLENSLFTLTPLTAGSETAFVTDFW-NEEFGVPGAFIKNTHINEFFLKSLTLE 130
Qy 131 DVPNHGKVHFCNSWYVPANKYKSDRIFFANQAYLPSETPTLTKRYRENELVTLRGDGTG 190
Db 131 DVPNHGKVHFCNSWYVPFRYKSDRIFFVNPQVLPSTPELLARKYRENELLTLRGDGTG 190
Qy 191 KLEWDRVYAYVNDLGDGPKGQDLSRPVLGGSSSEYPPRRGRTGRKPTKTDNSESRI 250
Db 191 KREAWDRYDYINDLGNPDGKENVRTTLGSAEYPPRRGRTGRPTTRTDPKSESRI 250
Qy 251 PLLMSLDIYVPRDERFGHILKSDPLTEALKSIQVLLLPFKALFQSTHNEEDSPEDVLKL 310
Db 251 PLILSLDIYVPRDERFGHLKMSDPLTALKSIVQFILPELHALFDGTFNEPDSFEDVLRL 310
Qy 311 YEGGIKLPQGLPKAKITDSIPLEILKELLRSDGELPKYPTTPQVIOEDKTAWRTDEEFG 370
Db 311 YEGGIKLPQGLPKAKITDSIPLEILKELLRSDGELPKYPTTPQVIOEDKTAWRTDEEFG 370
Qy 371 EMLAGVNPVITISRLQRPFPKSKLDPKIYGNQNSITIREQIEDKLDGLTIDRAIKTNRLFI 430
Db 371 EMLAGVNPVITISRLQRPFPKSKLDPEAYGNQNSITIAEHIEDKLDGLTIDRAIKTNRLFI 430
Qy 431 LNHHDLMPVLRINTSTDTKYASRTLLFDQNGTLKPSAIELSLPHDPDGDQFCAVSKV 490
Db 431 LNHHDLMPVLRINTSTDTKYASRTLLFDQNGTLKPSAIELSLPHDPDGDQFCAVSKV 490
Qy 491 YTPADQGVGSIWQAKAYAVNDSGVHQLTISHWLNTAAIEPFIATNRQSLALHPIYK 550
Db 491 YTPADQGVGSIWQAKAYAVNDSGVHQLTISHWLNTAAIEPFIATNRQSLALHPIYK 550
Qy 551 LLHPHRETNNINARQILINGGLLELVFPKAYSNMGSVAVYKQWVFPQALPTDLI 610
Db 551 LLHPHRETNNINARQILINGGLLELVFPKAYSNMGSVAVYKQWVFPQALPTDLI 610
Qy 611 KRGVAVEDSSPLGIRLLIODYPVAVDGLKTWSAKSVTEYCNVYKSDDAVOKDTLQ 670
Db 611 KRGVAVEDSSPLGIRLLIODYPVAVDGLKTWSAKSVTEYCNVYKSDDAVOKDTLQ 670
Qy 671 AWWKELREGEHGDKKDEPWPMPKMTVQELIDSCITTIWIASALHAANVFGQYPVAGYLPN 730
Db 671 AWWKELREGEHGDKKDEPWPMPKMTVQELIDSCITTIWIASALHAANVFGQYPVAGYLPN 730
Qy 731 RPTLSRNFMPGSPGYEELKTNPKVFLKTIIPOLQTLGSLIELSRHSSDTLYLGQ 790
Db 731 RPTLSRNFMPGSPGYEELKTNPKVFLKTIIPOLQTLGSLIELSRHSSDTLYLGQ 790
Qy 791 RESPEWTKDQEPISAFARFGKKISDIEDQIMQMNVDKWNRSRGPVVPYTLFPPTSEG 850
Db 791 RESPEWTKDQEPISAFARFGKKISDIEDQIMQMNVDKWNRSRGPVVPYTLFPPTSEG 850
Qy 851 LTGKIPNSVSI 862
Db 850 LTGKIPNSVSI 861

RESULT 10
ID O9SC16 PRELIMINARY; PRT; 861 AA.
AC O9SC16;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).

Db	311	YEGGIKUQPGQLFKALFAALPLEMIRELLRTDGBGILRFPPTPLVTKOSKTAWRTDEEFAR	370
Qy	371	EMLAGVNPVPIISRLQEPFPKSKLDPKIQNGQNSITTRREQIEDKLDGLTIDEAIKTNRLFI	430
Db	371	EMLAGVNPPIIISRLQEPFPKSKLDPKIQNGQNSITTAEHIEDKLDGLTIDEAMNNKLEI	430
Qy	431	LNHHDIIMPYLRIINTSDTKTYASRTLLFLQDNGTLKPSAIEISLPHDPGQDFGAVSKV	490
Db	431	LNHHDIIPYLRINT-TITKTYASRTLLFLQDNGSLKPLAIEISLPHDPGQDFGVTSKV	489
Qy	491	YTPADQCEGSIWOLAKAYAVNDGSHVHLSHNLTHAAIEPPVIATNRQLSALHPPIYK	550
Db	490	YTPSDQGVESSIWOLAKAYAVNDTGVHQLISHNLTHAVIEPPVIATNRQLSVLHPPIHK	549
Qy	551	LLPHFPRETWNINARQIILINGGGLLELTVFPKAKYSMEMSAVVYKDWVFPQALPTDLI	610
Db	550	LLYPHFEDTWNINASARQILVNAGGVLESTVFQSKFAMEMSAVVYKDWVFPQALPADLV	609
Qy	611	KRGVAVEDSSPGLIRLLIQDYPAVDGLKTIWSAISKSWTVCNYYKSDDDAVQKDTLQ	670
Db	610	KRGVAVEDSSSPGHVRLIEDYPAVDGLTIWSAISKSWTVCNYYKSDDEILKDNELQ	669
Qy	671	AWKKEIREEGHGDKDEPMPKQTVQELIDSCITTIWIASALHAAVNFQYPAAGYLPN	730
Db	670	AWKKEIREVGHGDKKNPMPKQTVQELIDSCITTIWIASALHAAVNFQYPAAGYLPN	729
Qy	731	RPTLSRNFMPPEGSPYEELKTNPKVFLKTIITPQLOTLGILSIEILSRHSSDTLYLQ	790
Db	730	RPTVSRRFMEPGTDEELKRNPKAFKLTITAQLTQLGVSILSRHTTDEIYLQ	789
Qy	791	RESPWTKDQEPISAFARFGKGLSDIEDQIMQMVDEKWNKRSQGVKYPTLLPFTSEGG	850
Db	790	RESPWTKDKEPLAAPDRFGKGLTDEKQIIQRNGDNLTKRSGPVNAPYTLLPFTSEGG	849
Qy	851	LTGKGIPNSVSI 862	
Db	850	LTGKGIPNSVSI 861	

RESULT 11

O22508 PRELIMINARY; PRT; 861 AA.

AC O22508

AC 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Lipoxigenase.

GN Name=plox2;

OS Solanum tuberosum (potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Solanales; Solanaceae; Solanum.

ON NCBI_TaxID=4113;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Lehm Russel; TISSUE=Tuber;

RA Fidantsef A.L., Bostock R.M.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Plant lipoxigenase may be involved in a number of

CC diverse aspects of plant physiology including growth and

CC development, pest resistance, and senescence or responses to

CC wounding (By similarity).

CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -1- COFACTOR: Iron (By similarity).

CC -1- SIMILARITY: Belongs to the lipoxigenase family.

CC -1- SIMILARITY: Contains 1 PLAT domain.

DR EMBL; AF019614; AAB81595.1; --

DR HSSP; P08170; 1FGT

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016165; F:lipoxigenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.


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Db 134 DVPHGKVFHDCNWSWYPSFRYKSDRIFFANOPYLPSKTPPELLRYKRENEELLTLRGDGTG 193
Qy 191 KLEEDRWVYDYANDLGDPPDQDGLSRVVLGSSSEYPPVPRGRGCRKTKTDPNSESRI 250
Db 194 KREAMDRIYDIYDNLGPNDDQKENVRTTLGGSABEYPPRGRGTRPPRTDTPKSESRI 253
Qy 251 PLMSLDIYVPRDERFGHIKJSDFLTFALKSIVQLLPEFKALFDSTHNEFDSFEDVLKL 310
Db 254 PLLSLDIYVPRDERFGHLKMSDELTYALKSIVQFLPELHALFDGTPNEFDSFEDVLRL 313
Qy 311 YEGGKILPQGPLLKALTDISPILEIKELLRSDBGLFKYPTTQVTOEDKTAWRTDEEGR 370
Db 314 YEGGKILPQGPLFKALTAIPLEMIKELLRTDGEGLRPTPLVTKDSKTAWRTDEEFA 373
Qy 371 EMLAGVNPVIRLOEFPPKSKLDPKIKYGNQNSTITREOIEKLDGLATIDEAKTNRLFI 430
Db 374 EMLAGVNPVIRLOEFPPKSKLDPEYGNQNSTITAEHIEDKLDGLTVDEANNKLUFI 433
Qy 431 LNHHDILMPYLRRINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHDPDQDQFGAVSKV 490
Db 434 LNHHDILPILRRINT-TITKYSASRTLLFLQDNGSLKPELAIELSLPHDPDQDQFGVTSKV 492
Qy 491 YTPADQGVGSGTWOLAKAYAVANDSGVHQLISHWLNTHAIEPFIATNRQLSALHPIYK 550
Db 493 YTPDQGVGESSIWOLAKAYAVANDAGVHQLISHWLNTHAVIEPFIATNRQLSVLHPHK 552
Qy 551 LHPHFRMTNINARQILINGGLLELTVPKYSWEMSAVYKDWVPEQALPTDLI 610
Db 553 LHPHFRMTNINARQILINAGVLESTVQSKFALEMSAVYKDWVFPQALPADLV 612
Qy 611 KRGVAVEDSSPLGLRLITQDYPYAVDGLKIWSAISKSWTEYCNVYKSDDAVQKDTLQ 670
Db 613 KRGVAVEDSSPHGVRLIEDYPAVDGLIWSAISKSWTDYCSFYGSDEILKDNELQ 672
Qy 671 AWWKELREHGDKKDEPWPQKQVTVQELIDSCITTIWIASALHAANFQVYAGYLPN 730
Db 673 AWWKELREVGDKKNEPWPMEPTQELIDSCITTIWIASALHAANFQVYAGYLPN 732
Qy 731 RPTLSRNWPEPGSPYEELKTNPKVFLKTTTPOLTLLGLSLIEILSRHSDTYLQ 790
Db 733 RPTVSRNPEPGTPEYELKKNPKAFUKTTTQOLTLLGSVLIELSRHTDIBYILQ 792
Qy 791 RESPTWKDQEPPLSFAFGKLSIDIEQIMQNVNDEKWNKSGVQVYPTLLPFTSEGG 850
Db 793 RESPTWKDQEPPLAFAFGKLTIEKQIIQNGDNILTRSGPNAPYTLTFTSEGG 852
Qy 851 LTGKIPNSVSI 862
Db 853 LTGKIPNSVSI 864

RESULT 13
LOXI_SOLTU STANDARD; PRT; 861 AA.
AC P37831;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipoxigenase 1 (RC 1.13.11.12).
GN Name=LOXI.1; Synonyms=LOX1;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree; TISSUE=Tuber;
RX MEDLINE=95175602; PubMed=7870815; DOI=10.1104/pp.107.1.265;
RA Casey R.;
RT "Sequence of a cDNA clone encoding a potato (Solanum tuberosum) tuber
lipoxigenase."
RL Plant Physiol. 107:265-266 (1995).

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CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence of responses to
CC wounding. It catalyzes the hydroperoxidation of lipids, containing
CC a cis,cis-1,4-pentadiene structure.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienolate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; X79107; CA455724.1; -
CC PIR; S44940; S44940.
CC HSSP; P08170; 1FGT.
CC InterPro; IPR000907; Lipoxigenase.
CC InterPro; IPR001024; Lipoxigenase LH2.
CC InterPro; IPR001246; Plant_lipoxynase.
CC InterPro; IPR008976; PLAT_LH2.
CC Pfam; PF00305; Lipoxigenase; 1.
CC Pfam; PF01477; PLAT; 1.
CC PRINTS; PR00087; LIPOXYGENASE.
CC PRINTS; PR00468; PLTPOXGNASE.
CC SMART; SM00308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
CC PROSITE; PS50095; PLAT; 1.
CC DiOxygenase; Iron; Multigene family; Oxidoreductase.
CC DOMAIN 29 160 PLAT
CC METAL 522 522 Iron (By similarity).
CC METAL 527 527 Iron (By similarity).
CC METAL 713 713 Iron (By similarity).
CC METAL 861 861 Iron (By similarity).
CC SEQUENCE 861 AA; 96966 MW; 09732A6751DEE20D CRC64;

Query Match Similarity 80.1%; Score 3632.5; DB 1; Length 861;
Best Local Similarity 78.9%; Pred. No. 1.7e-233;
Matches 672; Conservative 83; Mismatches 94; Indels 3; Gaps 3;

Qy 12 GKDGKKVKGTWLMKKNVLDFTDINASVLDGVLEFLGRRVSLISSVNADPPANGLOK 71
Db 12 GHDSKKVKGTVMNMKNVLDFTDLAGSLTKGIFDVLGQKVSFOLISSVQGDPTNGLOK 71

Qy 72 RSKAAYLENWLTNSTPIAAG-ESAPRVTFDWDDEFGVPGAFIINKLHFSFFFLKSLTLE 130
Db 72 HSNPAXLENSLFTLTPLTAGSETAFGVTFDW-NEEFGVPGAFIKNMHINEFFLKSLE 130

Qy 131 DVPHGKVFHDCNWSWYPSFRYKSDRIFFANOPYLPSKTPPELLRYKRENEELLTLRGDGTG 190
Db 131 DVPHGKVFHDCNWSWYPSFRYKSDRIFFANOPYLPSKTPPELLRYKRENEELLTLRGDGTG 190

Qy 191 KLEEDRWVYDYANDLGDPPDQDGLSRVVLGSSSEYPPVPRGRGCRKTKTDPNSESRI 250
Db 191 KREAMDRIYDIYDNLGPNDDQKENVRTTLGGSABEYPPRGRGTRPPRTDTPKSESRI 250

Qy 251 PLMSLDIYVPRDERFGHIKJSDFLTFALKSIVQLLPEFKALFDSTHNEFDSFEDVLKL 310
Db 251 PLLSLDIYVPRDERFGHLKMSDELTYALKSIVQFLPELHALFDGTPNEFDSFEDVLRL 310

Qy 311 YEGGKILPQGPLLKALTDISPILEIKELLRSDBGLFKYPTTQVTOEDKTAWRTDEEGR 370
Db 311 YEGGKILPQGPLFKALTAIPLEMIKELLRTDGEGLRPTPLVTKDSKTAWRTDEEFA 370

Qy 371 EMLAGVNPVIRLOEFPPKSKLDPKIKYGNQNSTITREOIEKLDGLTIDEAKTNRLFI 430

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Db 371 EMLAGNVPIISRLQEFFPKSKLDPEAGNQNSTIAEHIEDKLDGLTVDAMNNKLF 430
Qy 431 LNHHDLMPYLRINTSTDTTYASRTLLFLQDNGTLKPSAIEISLPHDPDQDQGVASKV 490
Db 431 LNHHDLMPYLRINT-TITKAYASRTLLFLQDNGSLKPLAIELSFPHDPDQDQGVTSKV 489
Qy 491 YTPADQGVGSSWOLAKAYAAVNDGSHVHQLISHWLNTHAAIEPFIATNROLSALHPYK 550
Db 490 YTPDQGVGSSWOLAKAYAAVNDGSHVHQLISHWLNTHAVIEPFIATNRQLSVLHPHK 549
Qy 551 LLHPHFRMTMINALARQILINGGLLELTVFPKAYSMEMSAVVYKDWVFPQALPTDLI 610
Db 550 LLYPHFRMTMINASARQLLNAGVLESTVFSKFAEMSAVVYKDWVFPDQALPADLV 609
Qy 611 KRGVAVEDSSPLGIRLLIQYPIYAVDGLKISWAIKSWWTCYNYKSSDVAQKDTLQ 670
Db 610 KRGVAVEDSSPHGVRLIEDYPIYAVDGLKISWAIKSWWTCYNYKSSDVAQKDTLQ 669
Qy 671 AWWKELREHGDKKDEPWPQWOTVQELIDSCITTIWIASALHAANFQYPIYAVLPN 730
Db 670 AWWKELREHGDKKDEPWPQWOTVQELIDSCITTIWIASALHAANFQYPIYAVLPN 729
Qy 731 RPTLSRNFWPSPGSEYELKTNPKVFLKTTIPOLQTLGSLTEILSRHSSDTLYLQ 790
Db 730 RPTVSRFPWPECTEYELKTNPKVFLKTTIPOLQTLGSLTEILSRHSSDTLYLQ 789
Qy 791 RESPEWTKDQPLSAFARFGKLSLSDIEDQIMQNVNDEKRNKRGPKVYPTLLFPTSEGG 850
Db 790 RESPEWTKDQPLSAFARFGKLSLSDIEDQIMQNVNDEKRNKRGPKVYPTLLFPTSEGG 849
Qy 851 LTGKGIPNSVSI 862
Db 850 LTGKGIPNSVSI 861

RESULT 14
Q42873 PRELIMINARY; PRT; 859 AA.
AC Q42873;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN Name=Lox;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN= Rutgers; TISSUE= Fruit pericarp;
RX MEDLINE=95241637; PubMed=7724686; DOI=10.1104/pp.107.2.669;
RA Kausch K.D., Handa A.K.;
RT "Molecular cloning and nucleotide sequence of a lipoxigenase cDNA from
RT ripening tomato fruit.";
RL Plant Physiol. 107:669-670(1995).
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; U13691; AA074393.1; -
DR PIR; T06352; T06352.
DR HSP; P09186; I003.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
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DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR001246; Plant_lipoxynase.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTLPXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00881; LIPOXYGENASE_2; 1.
DR PROSITE; PS00895; PLAT; 1.
DR Dioxigenase; Oxidoreductase.
SQ SEQUENCE 859 AA; 97136 MW; 738DE7E07A0793C8 CRC64;

Query Match 80.0%; Score 3625.5; DB 2; Length 859;
Best Local Similarity 79.4%; Pred. No. 4.8e-233;
Matches 685; Conservative 70; Mismatches 103; Indels 5; Gaps 3;

Qy 1 MFLEKIYDAITGKDDGKKVGTIVLMKKNVLDFTDINASVLDGVLEFLGRVSVLELIS-S 59
Db 1 MSLGGIVDALIGKDDRPKVRVILMKKNVLDFTINIGASVVDGISDLGKQVSIQLISGS 60
Qy 60 VNADPANGLOGKRSKAAAYLENWLTNSTPIAAGESAFRTVDWDDDEFGVPGAFIKNLHF 119
Db 61 VNYD---GLEKLSNPAYLESWLTIDTIPITAGESTFSVTFDWRDDEFVPGAFIKNLHL 117
Qy 120 SEFLKSLTLEDVPHGKHVFCNWSWYVPAKYKSDRIFFANQAYLPSETPTTLRKYREN 179
Db 118 NEFLKSLTLEDVPHGKHVFCNWSWYVPAKYKSDRIFFANQAYLPSETPTTLRKYREN 177
Qy 180 ELVTLRGDGTGLBEWDVYDYAYNDLGDQDKQDLSPVLCSSSEYVPRRTGRTGKP 239
Db 178 ELVALRGDGTGLBEWDVYDYACYNLGDGEPDKGEYARPILGSSSEYVPRRTGRTGEP 237
Qy 240 TKTDPNSESRIPLMSLDIYVPRDERFCHIKLSDFLTALKSIVOLLLPEKALFDSHTN 299
Db 238 TKADPNCESRNPLPMSLDIYVPRDERFCHVKKSDFLTSSLSLQTLPAFKALCDNTPN 297
Qy 300 EFDSEFVLYKLYEGGIKLPOGPLLKAITDSIPLBELKELRSDEGLFKYPTPOVIOBDK 359
Db 298 EFNSEFADVLYKLYEGGIKLPEGPMLKAITDNISSEILKDLQTDGGLKYPTPOVIOBDK 357
Qy 360 TAWETDEFEGRMLAGVNPVILSLOFPFKSLDKPKTYGNQNSTITREQLDKLGLTI 419
Db 358 TAWETDEFEGRMLAGVNPVILSLOFPFKSLDKPKTYGNQNSTITTEHVQDKLGLTV 417
Qy 420 DEAKTNRLFTLNHHDILMPYLRINTSTDTKYASRTLLFLQDNGTLKPSAIEISLPHP 479
Db 418 NEAKSNRLFTLNHHDIVMPLLRKINMSANTKAYASRTLLFLQDRTLKPLAIELSLPHP 477
Qy 480 DGDQFGAVSKYVTPADQGVGSIWOLAKAYAAVNDGSHVHQLISHWLNTHAAIEPFIATN 539
Db 478 DGDQFGTVSKYVTPADQGVGSIWQFAKAYAVNDMGTHQLISHWLNTHAVIEPFIATN 537
Qy 540 RQLSALHPYKLLHPHRETMINALARQILINGGLLELTVFPKAYSMEMSAVVYKDWV 599
Db 538 RHLVSLHPHPIHKLHPHFRMTMINALARETITYDGG-FETSLFFPAKYSMEMSAVVYKDWV 596
Qy 600 FPEQALPTDLTKRGVAVEDSSPLGIRLLIQYPIYAVDGLKISWAIKSWWTCYNYKSS 659
Db 597 FPEQALPADLLKRGVAVEDLSSPHGIRLLILDYPIYAVDGLKISWAIKSWWTCYNYKSS 656
Qy 660 DDVQKOTELQAWNKELREHGDKKDEPWPQWOTVQELIDSCITTIWIASALHAANF 719
Db 657 DETVEKOTELQAWNKELREHGDKKDEPWPQWOTVQELIDSCITTIWIASALHAALHF 716
Qy 720 QQYDYGAVLPNRPTLSRNFMPGSPVEELKTPDKVFLKTTIPOLQTLGSLTEILS 779
Db 717 GLYSYAGVLPNRPTLSRNFMPGSPVEELKTPDKVFLKTTIPOLQTLGSLTEILS 776
Qy 780 RHSSDTLYLGQRESPEWTKDQPLSAFARFGKLSLSDIEDQIMQNVNDEKRNKRGPKV 839
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Db	777	RHASDEVILQORDSIETWKDEPLVAFERFGKMLSDIENRIMNHSKSNKNSGPNVNP	836
Qy	840	YTLIRPTSEGLTGKIPNSVSI	862
Db	837	YTLIRPTSEGLTGKIPNSVSI	859
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ID	Q43189	PRELIMINARY;	PRT; 861 AA.
AC	Q43189;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Lipoxigenase	(EC 1.13.11.12).	
GN	Name=POLX-1;		
OS	Solanum tuberosum (Potato).		
OC	Eukaryota; Viridiplantae;	Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta;	eudicotyledons; core eudicots; asterids;	
OC	lamids; Solanales;	Solanaceae; Solanum.	
OX	NCBI_TaxID=4113;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Koloniets M.V., Hannapel D.J., Gladon R.J.;		
RT	"Potato Lipoxigenase Genes Expressed During the Early Stages of		
RT	Tuberization (Accession Nos. U60200 and U60201) (PCR96-065).";		
RL	Plant Physiol. 112:446-446(1998).		
CC	!- FUNCTION: Plant lipoxigenase may be involved in a number of		
CC	diverse aspects of plant physiology including growth and		
CC	development, pest resistance, and senescence or responses to		
CC	wounding (by similarity).		
CC	!- CATALYTIC ACTIVITY: Lipoate + O(2) = (9Z,11E)-(13S)-13-		
CC	hydroperoxyoctadeca-9,11-dienoate.		
CC	!- COFACTOR: Iron (by similarity).		
CC	!- SIMILARITY: Belongs to the lipoxigenase family.		
CC	!- SIMILARITY: Contains 1 PLAT domain.		
DR	EMBL; U60200; AAB67858.1; -		
DR	HSP; P08170; 1FGT		
DR	GO; GO:0005506; F:iron ion binding; IEA.		
DR	GO; GO:0016165; F:lipoxygenase activity; IEA.		
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR000907; Lipoxigenase.		
DR	InterPro; IPR001024; Lipoxigenase_LH2.		
DR	InterPro; IPR001246; Plant_lipoxygase.		
DR	InterPro; IPR008976; PLAT_LH2.		
DR	Pfam; PF00305; Lipoxigenase; 1.		
DR	Pfam; PF01477; PLAT; 1.		
DR	PRINTS; PR00087; LIPOXYGENASE.		
DR	PRINTS; PR00458; PLTIPOXYGNASE.		
DR	SMART; SM00308; LH2; 1.		
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.		
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.		
DR	PROSITE; PS00095; PLAT; 1.		
KW	Dioxygenase; Oxidoreductase.		
SQ	SEQUENCE 861 AA; 96973 MW; 11AA977F04FF1C56 CRC64;		
Query Match 80.0%; Score 3625.5; DB 2; Length 861;			
Best Local Similarity 78.9%; Pred. No. 4.8e-233;			
Matches 672; Conservative 83; Mismatches 94; Indels 3; Gaps 3;			
Qy	12	GKDDGKKVGTVMKKKVLDFDINASVLDGVLGFLGRVSLLEISSVNADPANGLOK	71
Db	12	GHDSSKKVGTVMKKKVLDFDINASVLDGVLGFLGRVSLLEISSVNADPANGLOK	71
Qy	72	RSKAAYLENLWLNSTPIAAG-ESAFTVFDWDEBFGVGAFTIKNLHSEFFFLKSLTLE	130
Db	72	HSNPAYLENLWLNSTPIAAG-ESAFTVFDWDEBFGVGAFTIKNLHSEFFFLKSLTLE	130
Qy	131	DVPNHGKVHFCVNSWVYFANKYKSDRIFFANQAYLPSETPDTRLKRYRENELVLRGDGTG	190
Db	131	DVPNHGKVHFCVNSWVYFANKYKSDRIFFANQAYLPSETPDTRLKRYRENELVLRGDGTG	190

Qy	191	KLEWDRVYVAYNDLGDPOKQDLSRPLVGGSEYVYPRGRTRGRKFTKTDPNSESRI	250
Db	191	KREAWDRYVDIYNDLGNPDGKENVTTLLGSAEYVYPRGRTRGRKFTKTDPNSESRI	250
Qy	251	PLMLSDIYVPRDERFGHIKLSDFLTFAKLSVQLLLPEFKALPDSHTNPFOSFEDVLKL	310
Db	251	PLILSTDIVVPRDERFGHLKMSDFLTVALKSVIQILPELHALFDGTNPFSFEDVLR	310
Qy	311	YEGGKILPOGLLKAITSDISPLEILKELLRSDEGLFKYPTPOVIOEDKTARTDEEFCR	370
Db	311	YEGGKILPOGLLKAITSDISPLEILKELLRSDEGLFKYPTPOVIOEDKTARTDEEFCR	370
Qy	371	EMLAGVNVIIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAKTNRLFI	430
Db	371	EMLAGTNPVIIISRLQEFPPKSKLDPEAYGNQNSTITAEHIEDKLDGLTIDEAMNNKLF	430
Qy	431	LNHHDIMPYLRIRINTSDTKTYASRTLLFLQDNQTLKPSAIELSLPHDPDQGFQAVSKV	490
Db	431	LNHHDLLPYLRIRINT-TITKTYASRTLLFLQDNQSLKPLAIELSLPHDPDQGFQVTSKV	489
Qy	491	YTPADQGVESGIWOLAKAYAVVNDSGVHQLISHWLNTHAAIEPFFVIATNRQLSALHPIYK	550
Db	490	YTPDQGVESGIWOLAKAYAVVNDSGVHQLISHWLNTHAVIEPFFVIATNRQLSALHPIHK	549
Qy	551	LLHPHFRTMINALARQILINGGGLLELTVPPAKYSMEMSAVVYKDWVFPPEQALPTDLI	610
Db	550	LLYPHFRTMINALARQILINAGVFSTVQSFQFALEMSAVVYKDWVFPPEQALPADLV	609
Qy	611	KRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWTEYCNYYKSDDAVQKDTLQ	670
Db	610	KRGVAVEDSSSPHGVRLIEDYPYAVDGLIWSAISKSWTDYCSFYGSDIEILKDNELQ	669
Qy	671	AWKELREEGHDKKDEBPWPKMOTVQELIDSCITTIWIASALHAANVFGQYPYAGYLPN	730
Db	670	AWKELREVGHDKKNEPWPPEMETPQELIDSCITTIWIASALHAANVFGQYPYAGYLPN	729
Qy	731	RPTLSRNFMPEPGSPSEYBELKTNPKVFLKTTTPOQLTLLGSLTLEILSRHSSDTLYLQ	790
Db	730	RATVSRNFMPEPGTPEYBELKKNPKDKAFKXTITAOQLTLLGSLVLEILSRHTTDIYLQ	789
Qy	791	RESPWTKDQPLSAPARFGKLSIEDQIMQNMVDEKWKNSRSGPVKVPYTYLLPTSEGG	850
Db	790	RESPWTKDKEPLAADFQKGLTDIEQIIQRNGDNILTNRSRGPVNAFYTYLLPTSEGG	849
Qy	851	LTGKIPNSVSI	862
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Search completed: March 10, 2005, 19:02:04

Job time : 189 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:52:42 ; Search time 45 Seconds
(without alignments)
1429.944 Million cell updates/sec

Title: US-10-731-642A-1

Perfect score: 4534

Sequence: 1 MFLEKIVDAITGKDDGKKVK.....LPFTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3610	79.6	859	4	US-09-978-522-3
2	3576	78.9	862	4	US-09-978-522-1
3	2905	64.1	857	4	US-09-751-687-17
4	2779.5	61.3	864	4	US-09-810-268-3
5	2745.5	60.6	865	4	US-09-751-687-16
6	2680	59.1	862	4	US-09-751-687-9
7	2673	59.0	862	4	US-09-751-687-12
8	2656	58.6	839	4	US-09-751-687-15
9	2584.5	57.0	864	4	US-09-751-687-18
10	1746.5	38.5	901	4	US-09-714-767A-4
11	558.5	12.3	675	4	US-09-902-540-12713
12	546	12.0	674	4	US-09-949-016-5980
13	546	12.0	689	4	US-09-949-016-11692
14	537.5	11.9	677	3	US-09-061-768A-4
15	537.5	11.9	677	4	US-09-764-246-4
16	537	11.8	711	4	US-09-547-435-2
17	537	11.8	867	4	US-09-547-435-24
18	527	11.6	556	4	US-09-547-435-6
19	510.5	11.3	701	3	US-09-087-727-2
20	510.5	11.3	701	4	US-09-853-053-2
21	510.5	11.3	701	4	US-09-949-016-6026
22	496	10.9	676	3	US-09-061-768A-2
23	496	10.9	676	4	US-09-764-246-2
24	496	10.9	676	4	US-09-949-016-6027
25	496	10.9	679	4	US-09-949-016-8912
26	487	10.7	662	3	US-09-061-768A-25
27	487	10.7	662	4	US-09-764-246-25

28	469.5	10.4	663	4	US-09-641-638-653	Sequence 653, App
29	469.5	10.4	663	4	US-10-170-097-653	Sequence 653, App
30	450.5	9.9	615	4	US-09-547-435-10	Sequence 10, Appl
31	450.5	9.9	771	4	US-09-547-435-28	Sequence 28, Appl
32	441.5	9.7	582	3	US-09-413-814-83	Sequence 83, Appl
33	440.5	9.7	460	4	US-09-547-435-12	Sequence 12, Appl
34	414.5	9.1	692	4	US-09-252-991A-19668	Sequence 19668, A
35	390	8.6	291	4	US-09-547-435-14	Sequence 14, Appl
36	303.5	6.7	195	4	US-09-547-435-20	Sequence 20, Appl
37	266	5.9	489	4	US-09-547-435-4	Sequence 4, Appl
38	266	5.9	645	4	US-09-547-435-26	Sequence 26, Appl
39	256	5.6	334	4	US-09-547-435-8	Sequence 8, Appl
40	172.5	3.8	477	4	US-09-902-540-12721	Sequence 12721, A
41	133.5	2.9	139	4	US-09-547-435-18	Sequence 18, Appl
42	126.5	2.8	1309	4	US-09-975-413A-10	Sequence 10, Appl
43	119	2.6	69	4	US-09-547-435-16	Sequence 16, Appl
44	118.5	2.6	1589	3	US-09-356-952-4	Sequence 4, Appl
45	117.5	2.6	1788	2	US-08-962-284-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-978-522-3
; Sequence 3, Application US/09978522
; Patent No. 6787684
; GENERAL INFORMATION:
; APPLICANT: Descenzo, Richard
; APPLICANT: Ireland, Nancy
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera
; FILE REFERENCE: 29520/37890
; CURRENT APPLICATION NUMBER: US/09/978,522
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,220
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Vitis LOX 2
US-09-978-522-3

Query Match	79.6%	Score	3610	DB	4	Length	859
Best Local Similarity	76.9%	Pred. No.	0				
Matches	661	Conservative	106	Mismatches	91	Indels	2
Gaps	2						
Qy	3	LEKIVDAITGKDDGKKVGT	VVLMKKNVLDFTDINASVLDGVLEFLGRRVSLDELISVNA	62			
Db	2	IHSIVGAITGENDKKIKGT	VVLMKKNVLDFTDINASVLDGVLEFLGRRVSLDELISVNA	61			
Qy	63	DPANGLQCKRKAAYLENW	LNSPTIAAGESAFRVTFDWDDEEFQVGPAGFIKNIHFSEF	122			
Db	62	DPANGLQCKIKGPAYLED	MITTITSLTAGESAFKVTDFW-DEEIGEPGAFIIRNNHSEF	120			
Qy	123	FLKSLTLEDPVNHGKHFV	CNSWYYPANKYKSDRIFFAQAYLPSETPTDLRKYRENEV	182			
Db	121	YLRTLTLEDPVGRGRIH	FVCSWYYPQAQHYKTDRTVFTNTQYLPSETPGPLKRYEGEL	180			
Qy	183	TLRGDGTCKLEWDRVYD	YAYNDLGDPKDQSLSRPVLGGSSEYPYPRRGTRGKPKTK	242			
Db	181	NLRGDTGELKEWDRVY	YAYNDLGNDRDLKVARPVLGGSSEYPYPRRGTRGKPKTK	240			
Qy	243	DPNSESRIPLMSLDIYV	PRDRERFHGKLSDFLTALKSIVQLLPKALPDSHNEFD	302			
Db	241	DPNTESEPLVMSLNIYV	PRDRERFHGKLSDFLTALKSIVQLLPKALPDSHNEFD	300			
Qy	303	SFEDVILKYEGLKPGP	LKATDSTPLILKELLSDGEGLPKYPPTQVQEDKTAW	362			
Db	301	SFQVDVLDLYEGGIVK	PEGLPDKDKNIPLEMLKELVETDGEHLKFFMPQVKEKSAW	360			
Qy	363	RTDEEFGREMLAGNVP	VIISRLQBPFPKSKLDPKIYGNQNSITITREQIEDKLDGLTIDEA	422			

Db 361 RTDEFAEMLAGNVPVIRLLQEPFPPKSLDPVYGNQNSIYKEHLENHLDLTINEA 420
 Qy 423 IKTNRLFILNHHDLIMPYLRRINTSTDTKTIVASRTLLFLQDNGTLKPSAIELSLPHDPGD 482
 Db 421 MEKKRLFILNHHDLIMPYLRRINT-TSTKTIVASRTLLFLQDNGTLKPSAIELSLPHDPGD 479
 Qy 483 QFGAVSKVYTPADQGVESIWOLAKAYAVNDGSHVHOLI SHWLNTHAAIEFPVIATNRQL 542
 Db 480 KFGAVNKVYTPAENGVEGSIWOLAKAYAVNDGSHVHOLI SHWLNTHAAIEFPVIATNRQL 539
 Qy 543 SALHPIYKLLHPHFRFTWNNALAQIILINGGGLLELTVFPKYSMEMSAVVYKDWVPE 602
 Db 540 SVLHPHKLHPHFRFTWNNALAQIILINGGGLLELTVFPKYSMEMSAVVYKDWVPE 599
 Qy 603 QALPDLTKRGVAVEDSSPLGIRLLIQDYPAVDGLKIWSAISKWTEYCNYYKSDDA 662
 Db 600 QALPADLTKRGVAVEDSSPLGIRLLIQDYPAVDGLKIWSAISKWTEYCNYYKSDDA 659
 Qy 663 VOKDTELOAWKELREEGHGDKDEPMPKMTVOELIDSCITTIWIASALHAAVNFQY 722
 Db 660 VOKDTELOAWKELREEGHGDKDEPMPKMTVOELIDSCITTIWIASALHAAVNFQY 719
 Qy 723 PYAGVLPNRPPLSRNFMPEGSPYEELKTNPKVFLKTIIPQLQTLGSLIELLSRHS 782
 Db 720 PYAGVLPNRPPLSRNFMPEGSPYEELKTNPKVFLKTIIPQLQTLGSLIELLSRHS 779
 Qy 783 SDTLYLGQRESPEWTKDQEPISAFARFGKLSIDEDQIMQNVDEKWRSGPVKVPYTL 842
 Db 780 SDEVYLGQRTPEWTLDTTLPKAFKFGKRLADIEEMIIDRNGRERFKRNGVPKIPYTL 839
 Qy 843 LPPTSEGLTGKGIPIINSVSI 862
 Db 840 LYPTSEGLTGKGIPIINSVSI 859

RESULT 2
 US-09-978-522-1
 ; Sequence 1, Application US/0978522
 ; Patent No. 6787684
 ; GENERAL INFORMATION:
 ; APPLICANT: Descenzo, Richard
 ; APPLICANT: Ireland, Nancy
 ; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera
 ; FILE REFERENCE: 29520/37890
 ; CURRENT APPLICATION NUMBER: US/09/978,522
 ; PRIOR FILING DATE: 2001-10-16
 ; PRIOR FILING DATE: 2000-10-16
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 862
 ; TYPE: PRT
 ; ORGANISM: Vitis LOX 1
 US-09-978-522-1

Query Match 78.9%; Score 3576; DB 4; Length 862;
 Best Local Similarity 76.2%; Pred. No. 0;
 Matches 655; Conservative 109; Mismatches 94; Indels 2; Gaps 2;

Qy 3 LEKIVDAITGKDGKVKVGLMKNVLDFTDINASVLDGLVLEFGRVSLIELSSVNA 62
 Db 5 LLSIVSAITGENDKKIEGTIVLMKNVLDFTDINASVLDGLVLEFGRVSLIELSSVNA 64
 Qy 63 DPANGLQKRSKAAVLENWLTNSTPIAGSARFTVFDWDEFGVPGAFIKNLHSEF 122
 Db 65 DPANGLQKRSKAAVLENWLTNSTPIAGSARFTVFDWDEFGVPGAFIKNLHSEF 123
 Qy 123 FLKSLTLEDPVNHGKVFVCSNWTVPANKYKSDRIFFANQAVLPSETDTTKYRENEVL 182
 Db 124 YLRTLTLEDPVGRHIFVCSNWTVPANKYKSDRIFFANQAVLPSETDTTKYRENEVL 183

Qy 183 TLRDGTGKLEEDRWYDYAYYNDLGDQDLRSPVLGGSSSEYPYPRRGRTRGKPKTK 242
 Db 184 NLRDGTGKLEEDRWYDYAYYNDLGDQDLRSPVLGGSSSEYPYPRRGRTRGKPKTK 243
 Qy 243 DPNSERIPILMSLDIYVPRDERFGHKLSDFLTFALKSIVOLLPLPFKALFDSHNEFD 302
 Db 244 DPKTESRLPLVMSLNIYVPRDERFGHKLSDFLTFALKSIVOLLPLPFKALFDSHNEFD 303
 Qy 303 SFEDVLKYGEGIKLPOGPLLKAITDSIPLEIKELARSDEGLFKYPTPOVIOEDKTAW 362
 Db 304 SFQDVLKYGEGIKLPOGPLLKAITDSIPLEIKELARSDEGLFKYPTPOVIOEDKTAW 363
 Qy 363 RTDEFGREMLAGNVPVIRLLQEPFPPKSLDPVYGNQNSIYKEHLENHLDLTINEA 422
 Db 364 RTDEFGREMLAGNVPVIRLLQEPFPPKSLDPVYGNQNSIYKEHLENHLDLTINEA 423
 Qy 423 IKTNRLFILNHHDLIMPYLRRINTSTDTKTIVASRTLLFLQDNGTLKPSAIELSLPHDPGD 482
 Db 424 MEKKRLFILNHHDLIMPYLRRINT-TSTKTIVASRTLLFLQDNGTLKPSAIELSLPHDPGD 482
 Qy 483 QFGAVSKVYTPADQGVESIWOLAKAYAVNDGSHVHOLI SHWLNTHAAIEFPVIATNRQL 542
 Db 483 KFGAVNKVYTPAENGVEGSIWOLAKAYAVNDGSHVHOLI SHWLNTHAAIEFPVIATNRQL 542
 Qy 543 SALHPIYKLLHPHFRFTWNNALAQIILINGGGLLELTVFPKYSMEMSAVVYKDWVPE 602
 Db 543 SVLHPHKLHPHFRFTWNNALAQIILINGGGLLELTVFPKYSMEMSAVVYKDWVPE 602
 Qy 603 QALPDLTKRGVAVEDSSPLGIRLLIQDYPAVDGLKIWSAISKWTEYCNYYKSDDA 662
 Db 603 QALPADLTKRGVAVEDSSPLGIRLLIQDYPAVDGLKIWSAISKWTEYCNYYKSDDA 662
 Qy 663 VOKDTELOAWKELREEGHGDKDEPMPKMTVOELIDSCITTIWIASALHAAVNFQY 722
 Db 663 VOKDTELOAWKELREEGHGDKDEPMPKMTVOELIDSCITTIWIASALHAAVNFQY 722
 Qy 723 PYAGVLPNRPPLSRNFMPEGSPYEELKTNPKVFLKTIIPQLQTLGSLIELLSRHS 782
 Db 723 PYAGVLPNRPPLSRNFMPEGSPYEELKTNPKVFLKTIIPQLQTLGSLIELLSRHS 782
 Qy 783 SDTLYLGQRESPEWTKDQEPISAFARFGKLSIDEDQIMQNVDEKWRSGPVKVPYTL 842
 Db 783 SDEVYLGQRTPEWTLDTTLPKAFKFGKRLADIEEMIIDRNGRERFKRNGVPKIPYTL 842
 Qy 843 LPPTSEGLTGKGIPIINSVSI 862
 Db 843 LYPTSEGLTGKGIPIINSVSI 862

RESULT 3
 US-09-751-687-17
 ; Sequence 17, Application US/09751687
 ; Patent No. 6660915
 ; GENERAL INFORMATION:
 ; APPLICANT: Douma, Anneke
 ; APPLICANT: Doderer, Albert
 ; APPLICANT: Cameron-Mills, Verena
 ; APPLICANT: Skadhauge, Birgitte
 ; APPLICANT: Bech, Lene
 ; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
 ; FILE REFERENCE: 11225.11US01
 ; CURRENT APPLICATION NUMBER: US/09/751,687
 ; CURRENT FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 857
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 US-09-751-687-17

Query Match 64.1%; Score 2905; DB 4; Length 857;
 Best Local Similarity 63.3%; Pred. No. 1.3e-271;

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Matches 548; Conservative 122; Mismatches 160; Indels 36; Gaps 9;
QY 16 GKXVGTVMKKNVLDFT-----DINASVLDGVLEFLGRVSVLELSSVNA 62
Db 9 GHKIKGTVMKKNVLDVNVSVTSVGIIQGGDLVGLSTLDTLTAFLGRSVSILSATKA 68
QY 63 DPANGLOGRKSKAAVLENNWLTNSTPIAAGESAFRVTDFDWDDEFGVPGAFIKNLHSEF 122
Db 69 D-ANG-KGKLGKATPLEGIITSLPTLGAGSFAKINFENDGGS-GIPGAFYIKNFMQTEF 125
QY 123 FLKSLTLEDPVNHGKVHVCNSWVYPANKYKSDRIFPANOAYLPSETPTDLRYKRENEVL 182
Db 126 FLVSLTLEDIPNHGSHIFVCNSWVYNAKLKSDRIFPANOAYLPSETPTDLRYKRENEVL 185
QY 183 TLRGDGTGKLEWDRVYDYAYNDLGDGDPKQDLSRPVGLGSSSEYPPRRGTGRKPTKT 242
Db 186 NURGDGTGRKEWERIYDYVNDLGDGDPKGNHARFVLGGNDTFPPRRGTGRKPTKT 245
QY 243 DPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFALKSIVOLLPEFKALFD--STHNE 300
Db 246 DPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFALKSIVOLLPEFKALFD--STHNE 300
QY 301 FDSFEDVLKYGCGIKLPOGILLKAITDSI-----PLEIKELLRSDEGELFKYPTPOVITQ 356
Db 301 FDSFEDVLKYGCGIKLPOGILLKAITDSI-----PLEIKELLRSDEGELFKYPTPOVITQ 356
QY 357 EDKTAWRTDEEFGREMLAGVNPVILSRLOEFPKSKLDPKIYGNQNSTITREQIEDKLDG 416
Db 353 VSKSAMWTEDEEFAREMLAGVNPVILSRLOEFPKSKLDPKIYGNQNSTITREQIEDKLDG 416
QY 417 LTIDBAIKTNRLFILNHHDIIMPYLRINTSTDTKYASRTLLFLQDNGTLKPSAIELSL 476
Db 413 LTIDBAIKTNRLFILNHHDIIMPYLRINTSTDTKYASRTLLFLQDNGTLKPSAIELSL 476
QY 477 PHPDGQFQAVSKVYTPADQGVESGSIWOLAKAYAVNDSGVHOLISHWLNTHAAIEPPVI 536
Db 472 PHPDGQFQAVSKVYTPADQGVESGSIWOLAKAYAVNDSGVHOLISHWLNTHAAIEPPVI 536
QY 537 ATNRLSALHPYIKLHHPHRETMINALARQILINGGGLLELTVPPAKYSMEGSAVYK 596
Db 532 ATNRLSALHPYIKLHHPHRETMINALARQILINGGGLLELTVPPAKYSMEGSAVYK 596
QY 597 DWVFEQALPTDLIKRGVAVESDSSPLGIRLLITQYPAVADGLKIWSAISKSWTYECNY 656
Db 592 DWVFEQALPTDLIKRGVAVESDSSPLGIRLLITQYPAVADGLKIWSAISKSWTYECNY 656
QY 657 YKSDAQQKTELQAWKELREBEGHDKKDEPMPKMQTVOBELDSCITTIWIASALHAA 716
Db 652 YKSDAQQKTELQAWKELREBEGHDKKDEPMPKMQTVOBELDSCITTIWIASALHAA 716
QY 717 VNFQGYPYAGYLPNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPV 776
Db 712 VNFQGYPYAGYLPNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPV 776
QY 777 ILSRHSSTLYLGQRESPEWTKDQEPPLSAFARFGKLSIEDIEQIMQNVNDEKWKNSRGPV 836
Db 772 ILSRHSSTLYLGQRESPEWTKDQEPPLSAFARFGKLSIEDIEQIMQNVNDEKWKNSRGPV 836
QY 837 KVPYTLPTSGGTLGKIPNSVSI 862
Db 832 QMPYTLPTSGGTLGKIPNSVSI 857

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RESULT 4

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US-09-810-268-3
; Sequence 3, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use

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; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 864
; TYPE: PR1
; ORGANISM: Zea mays
; US-09-810-268-3

Query Match      61.3%; Score 2779.5; DB 4; Length 864;
Best Local Similarity 60.6%; Pred. No. 1.9e-259;
Matches 525; Conservative 124; Mismatches 207; Indels 11; Gaps 5;

QY 3 LEKIVDAITGKDDGKVKVGTVMKKNVLDFTDINASVLDGVLEFLGRVSVLELSSVNA 62
Db 2 LSGIIDGLTGANKHARKLGTVMKKNVLDLNDFGATVVDVSISEFLGKGTQCQLISSTLV 61
QY 63 DPANGLOGRKSKAAVLENNWLTNSTPIAAGESAFRVTDFDWDDEFGVPGAFIKNLHSEF 122
Db 62 DANNNGRGRVGAENLEQWLTSLPSLTTCESKFGVTFDWEVEKLGVPGAVVKNHAAEF 121
QY 123 FLKSLTLEDPVNHGKVHVCNSWVYPANKYKSDRIFPANOAYLPSETPTDLRYKRENEVL 182
Db 122 FLKSLTLEDPVNHGKVHVCNSWVYPANKYKSDRIFPANOAYLPSETPTDLRYKRENEVL 182
QY 183 TLRGDGTGKLEWDRVYDYAYNDLGDGDPKQDLSRPVGLGSSSEYPPRRGTGRKPTK 241
Db 182 NLRGDDQGPQYQEHDRVRYDYNDLGEPPDGN--PRPILGGSADHPYPRRCRTGRKPTK 239
QY 242 TDPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFALKSIVOLLPEFKALFDSTHNEF 301
Db 240 TDPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFALKSIVOLLPEFKALFDSTHNEF 301
QY 302 DSFEDVLKYGCGIKLPOGILLKAITDSI-----PLEIKELLRSDEGELFKYPTPOVITQ 361
Db 298 DSFEDVLKYGCGIKLPOGILLKAITDSI-----PLEIKELLRSDEGELFKYPTPOVITQ 361
QY 362 WRTDEEFGREMLAGVNPVILSRLOEFPKSKLDPKIYGNQNSTITREQIEDKLDGTTDE 421
Db 358 WRTDEEFGREMLAGVNPVILSRLOEFPKSKLDPKIYGNQNSTITREQIEDKLDGTTDE 421
QY 422 AIKTNRLFILNHHDIIMPYLRINTSTDTKYASRTLLFLQDNGTLKPSAIELSPHPDG 481
Db 418 ALDGNRLYILDHHRFMPFLIDVNNLEGNFIYATRTFLRGGDLAPLAIELSEFYIDG 477
QY 482 DQFGAVSKVYTPADQGVESGSIWOLAKAYAVNDSGVHOLISHWLNTHAAIEPPVIATNRQ 541
Db 478 DQFGAVSKVYTPADQGVESGSIWOLAKAYAVNDSGVHOLISHWLNTHAAIEPPVIATNRQ 541
QY 542 LSALHPYIKLHHPHRETMINALARQILINGGGLLELTVPPAKYSMEGSAVYKDWVP 601
Db 538 LSALHPYIKLHHPHRETMINALARQILINGGGLLELTVPPAKYSMEGSAVYKDWVP 601
QY 602 EQALPTDLIKRGVAVESDSSPLGIRLLITQYPAVADGLKIWSAISKSWTYECNYKSSD 661
Db 598 EQALPTDLIKRGVAVESDSSPLGIRLLITQYPAVADGLKIWSAISKSWTYECNYKSSD 661
QY 662 AVOKDELQAWKELREBEGHDKKDEPMPKMQTVOBELDSCITTIWIASALHAAVNFQ 721
Db 658 AVOKDELQAWKELREBEGHDKKDEPMPKMQTVOBELDSCITTIWIASALHAAVNFQ 721
QY 722 YPYAGYLPNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPV 781
Db 718 YPYAGYLPNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPVTLNRPV 781
QY 782 SSDTYLQGRESPEWTKDQEPPLSAFARFGKLSIEDIEQIMQNVNDEKWKNSRGPV 841
Db 778 SSDTYLQGRESPEWTKDQEPPLSAFARFGKLSIEDIEQIMQNVNDEKWKNSRGPV 841

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QY 842 LLFP-TSE-----GGLTGKIPNSVSI 862
Db 838 LLYPNTSDHSGAAGLTAKGIPNSISI 864

RESULT 5
US-09-751-687-16
; Sequence 16, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-16

Query Match 60.6%; Score 2745.5; DB 4; Length 865;
Best Local Similarity 59.6%; Pred. No. 3.7e-256;
Matches 526; Conservative 129; Mismatches 190; Indels 37; Gaps 11;

QY 1 MFELKIVDAITGKDDGKKVGTVMKKNVLDP-----TDIN--ASVLD 42
Db 1 MFSVPGVSGILNRGGHKIKGTVMKKNVLDNFNSVADLTGKNGVGLTGLNVVSGTLD 60

QY 43 GVLEFLGRVSVLELISVSNADPANGLOGKRSKAAVLENNLTNSTPIAAGESAFRTVTPDW 102
Db 61 NLTAFLGRSVALQLISAUK-PLANG-KGKVGKDTFLEGLIIVSLPTLGAGESAFNQFEM- 117

QY 103 DEFGVPGAFIKNHFSFEFFLKSUTLEVPNHGKHFVCSWVYVANKYKSDRIFFANQ 162
Db 118 DESMGIPGAFYIKNMVQVEFYLSLTLEVPNQGTIRFVCSWVYVANKYKSDRIFFANH 177

QY 163 AYLPSSETPTLRYENELVTRGGTGLBEWDVAVDYAYNDLGDQKQDLSPVLG 222
Db 178 TVPSETPAALVGYREEELNLRGDKGERKHDRIYDVYNDLGNPDHGFARFILG 237

QY 223 GSSEYPPRRGRTRKPTKTDPNSESRIPLMSLDIYVPRDRFRGHIKLSDFLTALKSI 282
Db 238 GSSTHPYPRGRTRGYPTRKQNSEK-----PGEVYVPRDENFGLKSSDFLAYIKSL 291

QY 283 VOLLPEPKALPD--STNNEPDSFEDVLKLYEGGKLPQGPLLKAITSDIPLLEIKELLR 340
Db 292 SQVLPAPESVFDLNTFNEPDSFDVRLDHEGGIKLP----TEVISTIMPLPVVKELFR 347

QY 341 SDEGLFKVPTQVTOEKTARNTDEEFGREMLAGNVPVLSRLQEPFKSLDKPKIYN 400
Db 348 TDGEQVLKFPVPHV1QVSKSAMTDEEFAREWAGVNPVIRGLQEPFKSLNLDPTIYGE 407

QY 401 QNSTTITREQIEDKLGITIDEAIKTNRLFILNHHILMPLRYLRINTSDTKTYASRTLLF 460
Db 408 QTSKITADALD--LDGYTVDEALASRLFLMDYDHFVMPYIRRN-QTYAKAYATRTILF 464

QY 461 LDQNGTLKPSALELSLPHDPDQFGAVSKVYTPADQGVGSIWOLAKAYAAVNDSGVHQL 520
Db 465 LRENGTLKPAVLELSLPHDPAGDLSGAVSQVILPAKEGVESTIWLAKAYAVVNDSCYHQL 524

QY 521 ISHLNTHAAIEPFVIATNRQISALHPYIKLHPHRETMINALARQILLINGGLELT 580
Db 525 MSHWLNTHAVIEPFVIATNRHLSALHPYIKLHPHRETMINALARQILLINGGLELT 584

QY 581 VPPAKYSMEMSAAVYKDWYFPFQALPTDLIKRGVAVEDSSSPGLIRLLITQDYFPAVDGLK 640
Db 582 KQAWRTDEFAREVLAVGNPVMTIRLTFFPPKSLDPSKFGDHTSTITAEHIEKLEGIT 411
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QY 843 LPFTSEG-----GLTKGIPNSVSI 862
Db 839 LYPNTSDHTGQAEGLTARGIPNSISI 864

RESULT 10
US-09-714-767A-4
; Sequence 4, Application US/09714767A
; Patent No. 6709865
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis
; APPLICANT: Duwick, Jon
; APPLICANT: Hendrick, Carol
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; APPLICANT: Crasta, Oswald
; TITLE OF INVENTION: Sunflower RhoGAP, LOX, ADH and SCIP -
; TITLE OF INVENTION: Polynucleotides and Methods of Use
; FILE REFERENCE: 35718/201902
; CURRENT APPLICATION NUMBER: US/09/714,767A
; CURRENT FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/166,128
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: US 60/201,837
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Helianthus annuus
US-09-714-767A-4

Query Match 38.5%; Score 1746.5; DB 4; Length 901;
Best Local Similarity 42.7%; Pred. No. 2.2e-159;
Matches 357; Conservative 148; Mismatches 283; Indels 49; Gaps 15;

QY 40 VLDGVLEFLGRVSLLELISSVNADPANGLOGKRSKAAVLENWLTNSTPIAAGESAFRTVF 99
Db 100 IDVGVSDLLGSLFLELSVN-DLDSKGNQKTAKARY-----NALDLDISVYTKCDF 152
QY 100 DWDDBEFGVPGAFIKNLHFSFFKLSLTLEDVPHGKVFHVCNSWVYPANKYKSDRIFF 159
Db 153 D-VPDFGEIGAVLENYSKQWPKFNIVL-----NNG-VTFCESWVHSKYDNPEKRIFF 206
QY 160 ANQAVLPSETPTLKYRENELVTLRGDTGKLEBWDVYVAYNDLGDPPKGDLSRP 219
Db 207 TDKSYLPLETPTALKPLREKDMESLRNGEGGRKSFERYDYDVYNDLGDPPDGLDLP 266
QY 220 VLGSSSEYPPRRGRGTGRKPTKTDPSBSRIPLLMSLDIYVPRDRFPGHILKSLDFLTAL 279
Db 267 VLGGET-HPYPRCTRGRKMSKDLPTESR-----TTLPPYVPADEDFSEIKSVNFGAKTL 321
QY 280 KSIQVQLLPEFKALPDSHTNEPDSFEDVLKYGEGIKLPOGP-----LLKAITDSI 330
Db 322 YSVLHGVPMLDSIVTDKDGPLTSDLLYNEGVNVPSPDNGILSALPLVKCATDA- 380
QY 331 FLEILKELLSRSGEGFLKYPTQVTOEDKTAWRTDEEFGREMLAGVNPVVISRLQEPFPPK 390
Db 381 -----ANTVIKFETPETIDRDAFSWFRDEEFCRQMLAGINPCRIQLVTEWPLM 428
QY 391 SKLDPKIYQNSNTTTRQIEDKLG-LTIDEAICTNRLFILNHHDLILMPYLRINTSTD 449
Db 429 SKLDPKIYGAESAITKEIVEEIEIGFTLEBALAQKLFMLDYHDLLPYNKK--TEAE 486
QY 450 TKT-YASRTLLPLQNGTLKPSAIELSLPHPDGQFGAVSKVYTPADQGVGSIWOLAKA 508
Db 487 GRTLYGSRFLMFLTPAGTLRPLAIELTPPVDDCKP--QWKAHYTTPAWDATGAWLWKLAKA 544
QY 509 YAAVNDSGVHQLISHLWNTAAIEPFVIATNRQLSALHPHPIYKLLPHPRETMNINALARQ 568
Db 545 HVLAHDSYHQLVSHLWTHCATPEYIIATNRQLSQMHPIRRFLLPHFRYTMQINSLARL 604

QY 569 ILINGGGLLELTVPFPAKYSMEMSAVVY-KDWVFPQALPTDILI KRGVAVEDSSSPLGIRL 627
Db 605 LLVNWANGIIESTFSRCYCMQISSDAYDQQRWFDEALPADLI SRGMAVEDTAPYGVKL 664
QY 628 LIQYPIYAVDGLKIWSAISKSWVTEYCNYYKSDDDAVQKDTLQAWKELREEGHGDKDE 687
Db 665 TIEDYPIYANDGLLIYDTIKQWATSVNHYVPPANLVESDEELQAWWNEIRTVGHGDKDE 724
QY 688 PWPXKQVQBELIDSCITTIWIASALHAANVFGQPYAGYLPNRLTSLRNFP--EPGSP 745
Db 725 PWPQLKTDLLIGIVSTILMWTSQHSANVFGQYDFAGYFPENRPTISRTKMPNEDPTDE 784
QY 746 EYEELKTNPKVFLKTIITPQLQTLIGISLIETLSRHSDDTLVLGQRESPEWTKDQEPISA 805
Db 785 EQSFIKEPEDALLKCFPSQIQATKVMAILDVLSSHSPDEEYIGGNIEAWEAEPAIKAA 844
QY 806 FARFGKLSIEDIQIMQNMVDEKMKRSGPVKPYVTLTLPFTSEGLTKGIPNSVSI 862
Db 845 FEEFRGLNELEAIIIDSRNTDPLNKNRSGAGLVYPYQLLKPYSEKVTGCRGVPNSISI 901

RESULT 11
US-09-902-540-12713
; Sequence 12713, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12713
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12713

Query Match 12.3%; Score 558.5; DB 4; Length 675;
Best Local Similarity 29.0%; Pred. No. 1.5e-44;
Matches 165; Conservative 102; Mismatches 214; Indels 87; Gaps 22;

QY 308 LKLYEGGKIKPOGPLLKAITD-SIPLEILKEL-----LRSDGEG- - - - -FKY-P 350
Db 156 LDLREGR-PLPKDELYRGLTEGSVEVVIATAKLNPLMTRAWNGLVDIFDFFKHLE 214
QY 351 TPQVIEDKTAWRTDEEFGREMLAGVNPVVISRLQEPFPPKSLDPKIYQNSNTTIREQI 410
Db 215 VPQLAQR---WKDLEFARQAVQGIAPLHITLVPSLP-----QGMPLTDDDV 258
QY 411 EDKLD-GLTIDEAICTNRLFILNHH--DILMPYLRINTSTDTKY--ASRTLLPLQNG 465
Db 259 RGLSPGTTALADAKRIFLIDFELIDDIRMYRKVGBDGEVEERRWAPAARCLLDDQOR 318
QY 466 TLKPSATLSLPHPDGQFGAVSKVYTPADQGVGSIWOLAKA VAVNDSGVHQLISHWL 525
Db 319 QLRPLATQLG-----RDAQKDPVTFENDDAYD---WLAAKIYRCSEGNHSHWVSHAL 368
QY 526 NTHAAIEPFVIATNRQLSALHPHPIYKLLPHPRETMNINALARQILINGGGLLE----LTVP 582
Db 369 RTHFVAFEPVWATWRNLPDPHPVYKLLRRFRYTLAINEGARKGLLDAGGVDFDIATGG 428
QY 583 PAKYSMEMSAVVYKDWVFPQALPTDILIKRGVAVEDSSSPLGIRLLIQDYAVDGLKIW 642
Db 429 PDKHLQLGKRGFORWTLADNKNRADLERRGVL-----DP-----AVLPNYPYRDDALFLW 479
QY 643 SAIKSWVTEYCNYYKSDDAVQKDTLQAWKELREEGHGDKDEPWPWKQTVQELIDS 702
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Db 480 DAFEYVGVGLRHFRTDADLEATEMOWKDLTE--HGLPVDKLPCLRELRVDDLDVI 537
Qy 703 CTTITWIASALHAANFGQYPYAGYLPNRPDLTSRNFMP-BFGSPYEYELKTNPKVFLKT 761
Db 538 LTTVLFTSVQHAANVLYQEHYAFVNPAPLSMRPRQKGTLRADI---PEMIPTKS 594
Qy 762 ITPQOTLLGLSLTEILSRHSDTYL---QORESPWTQDQPLSAFAPFGKLSIDIE 817
Db 595 -----QMLWQVAIGRALSGFQDEEYLHEGWRB--BYFHEPELVAIQRQERLRAOR 647
Qy 818 DQIMQMVNDKWKNRSGPVKPYTLLFP 845
Db 648 EAV-----EARNAGAEVPTILRP 666

RESULT 12
US-09-949-016-5980
; Sequence 5980, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5980
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5980

Query Match 12.0%; Score 546; DB 4; Length 674;
Best Local Similarity 25.0%; Pred. No. 2.4e-43;
Matches 197; Conservative 119; Mismatches 272; Indels 200; Gaps 27;

Qy 103 DEEFGVPGAFIKNLHF---SEFFLKSITLEDVPHNGKHFVCSWVYPANKYKSDRIFF 159
Db 59 DEELGEIQLVRIEKRYKWLNDNDWYLYTLK-TPHGDYIEFPYRWI-----104
Qy 160 ANQAYLPSETPTLRYRENELVTLRGDGTGKLEWDRVYAYYNDLGDPPKQDLSRP 219
Db 105 -----TGDV-----EVVLR-DGRAKLARDQDHIHLKQHR-----132
Qy 220 VLGSSEYPYPRGRGRTKPTKTPDNS-----ESRIPLLMSLDIY--VPRDEREGHIKL 271
Db 133 -----RKELETROKQYRWMEWNGFPLSDAKCHKDLPDIQDFSEKG 175
Qy 272 SDFLTFLKSIQVQLLPEFKALFDSHTNEFDSFDVLKLYEGGKILPOGPKLLKAITDSIP 331
Db 176 VDFVLNYSKAMENLFINRMEHMFQSSWDFADFEKIF-----VK-----ISNTIS 220
Qy 332 LEILKELLRSDEGLFKYPTPOVIEDKTAWTDEFGREMLAGNVPVILSRLOFPKPS 391
Db 221 ERMVNH-----WQEDLMFGYQFLNGCNVPLIRCTELPEK- 255
Qy 392 KLDPKIYGNQNSITREQIEDKLD-GLTIDEAKTNRLFILNHHDLMPYLRINTSTDT 450
Db 256 -----LPVTTEWVCSLEQLSLEQVQGNFIVDFE--LLDGIDANKTDPT 302
Qy 451 KTYASRTLLFLQDNGTLKPSATELSLPHDPDQFOGAVSKVYTPADQVEGSGTWOLAKAYA 510
Db 303 LQFLAAPICLLYKNLANKIVPIAQLNQIPGDE---NPILFPLSDAKYD---WLLAKITW 355
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Qy 511 AVNDSGVHQLISHLWNTHAAIEPVIATNRQLSALHPIYKLLHPHRETMINALARQIL 570
Db 356 RSSDFHVHQITHLRLTHLVSEVFGIANYQLPAVHIFKLLVAHVFTTAINTKAREQL 415
Qy 571 I-----NGGGLLELTVPFPAKYSMEMSAAVVYKDWVFPQALPTDLIKRGVAVED 618
Db 416 ICEGGLFDKANATGGGGHVQWV-----QRAMKDLTVASLCFPEA-----IKARGMESKE 464
Qy 619 SSSPLGRLLIODYPYAVDGLKIWSAISKSWTEVCNYYKSDDAVQKDTLQANWKELRE 678
Db 465 D-----IPYFYRDDGLLWVEAIRTTAEVVDIYYEGDQVVEEDPELQDFVNDVYV 515
Qy 679 EGHGDKDEPWPQKQVQELIDSCITITWIASALHAANFGQYPYAGYLPNRPDLTSRNF 738
Db 516 YGMRGRKSSGFPKSVKSRQLESEYLTVTVIFTASQAHAANFGQYDWCWISNAPPTWR-- 573
Qy 739 MPEP---GSPEYEEELKTNPKVFLKTITPQOTLLGLSLTEILSRHSDTYLQOESRPE 795
Db 574 APPPTAGVVTIEQI-----VDTLPDRGRSCHWLGAVWALSQFOENELFLGM--YPE 623
Qy 796 WTKDQEPD-SAFARFGKLSIDIEQIMQMVNDKWKNRSGPVKPYTLLPPTSSEGLTGK 854
Db 624 EHTEKPVTEAMARFRKNLEAIVSIAERNKK-----QLPYLYLSPDR-----667
Qy 855 GIPNSVSI 862
Db 668 -IPNSVAI 674

RESULT 13
US-09-949-016-11692
; Sequence 11692, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11692
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11692

Query Match 12.0%; Score 546; DB 4; Length 689;
Best Local Similarity 25.0%; Pred. No. 2.5e-43;
Matches 197; Conservative 119; Mismatches 272; Indels 200; Gaps 27;

Qy 103 DEEFGVPGAFIKNLHF---SEFFLKSITLEDVPHNGKHFVCSWVYPANKYKSDRIFF 159
Db 74 DEELGEIQLVRIEKRYKWLNDNDWYLYTLK-TPHGDYIEFPYRWI-----119
Qy 160 ANQAYLPSETPTLRYRENELVTLRGDGTGKLEWDRVYAYYNDLGDPPKQDLSRP 219
Db 120 -----TGDV-----EVVLR-DGRAKLARDQDHIHLKQHR-----147
Qy 220 VLGSSEYPYPRGRGRTKPTKTPDNS-----ESRIPLLMSLDIY--VPRDEREGHIKL 271
Db 148 -----RKELETROKQYRWMEWNGFPLSDAKCHKDLPDIQDFSEKG 190
Qy 272 SDFLTFLKSIQVQLLPEFKALFDSHTNEFDSFDVLKLYEGGKILPOGPKLLKAITDSIP 331
Db 191 VDFVLNYSKAMENLFINRMEHMFQSSWDFADFEKIF-----VK-----ISNTIS 235
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QY 332 LEIKELLSDGEGFKYPTPOVEDKTAWRTDEBFGREMLAGVNPVILSRLEPPPKS 391
 Db 236 ERVNH-----WEDLMFGYQFLNGCNPVILIRCTELPEK- 270
 QY 392 KLDPKIYQNSITITREQIEDKLD-GLTIDEAKTNRLFILNHHIDILPMLRINTSTDT 450
 Db 271 -----LPVTTEMVECSLERQSLSEQEQOQNIPIVDPE--LLDGIDANKTDPCT 317
 QY 451 KTYASRTILFLODNGTLKPSATELSLPHDPDGOFGAVSKVYTPADQGVGSGTWOLAKAYA 510
 Db 318 LOFLAAPICLLYKNLANKIVPITAIQLNQIPGDE---NPIFLPSDAKYD---WLLAKIIV 370
 QY 511 AVNDSGVHOLISHLNLTHAAIEPFIATNRQLSALHPIVKLLHPHRETMNINALARQIL 570
 Db 371 RSDDFVHQTIHLRLTHLVSEVFGIATYRQLPVAPHPFLLVAHVFTIAINTKAREQL 430
 QY 571 I-----NGGGLLELVFPKAYSMEMSAVVYKDWVPEQALPTDLIKRGVAVED 618
 Db 431 ICEGGLFDKANATGGGHQMV-----QAMKDLTYASLCFPEA-----IKARGMESKE 479
 QY 619 SSSPIGIRLLIODYPANDGLKIWSAKSWVTEYCNYYKSDDAVOKDTLOAWKELRE 678
 Db 480 D-----IPYFYRDDGLLWAEARTFTAEVVDIYEGQVVEDEPELODFVNDVTV 530
 QY 679 EGHGDKDPMPKMTVOELIDSCITITWIASALHAAVNFQYVPYAGVLPNRPILSRNF 738
 Db 531 YOMGRKSGFPKSVKSRQSLSEYLVITFTASAQAAVNFQYDWCWIPNAPPTMR-- 588
 QY 739 MPEP---GSPEYEELKTNPKVFLKTTITPOLQTLGISLIEILSRHSSDTLYIGORESPE 795
 Db 589 APPTAKGVVITIEI-----VDTLPDRGRSCHLGAVALSQOENELFLGM--YFE 638
 QY 796 WTKDQEPK-SAFARFGKLSLIEDQIMQNVDEKKNRSGPVKVPYTLPTSEGLTK 854
 Db 639 EHFIEKPVKEAMARFKNLAEIVSIAERNKKK-----QLPYLSPDR----- 682
 QY 855 GIPNSVSI 862
 Db 683 -IPNSVAI 689

RESULT 14
 US-09-061-768A-4
 ; Sequence 4, Application US/09061768A
 ; Patent No. 6204037
 ; GENERAL INFORMATION:
 ; APPLICANT: BRASH, ALAN R.
 ; APPLICANT: BOEGLIN, WILLIAM E.
 ; APPLICANT: JISAKA, MITSUO
 ; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: ARLES A. TAYLOR, JR.
 ; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
 ; CITY: DURHAM
 ; STATE: NORTH CAROLINA
 ; COUNTRY: USA
 ; ZIP: 27707
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
 ; COMPUTER: IBM PC/XT/AT compatible
 ; OPERATING SYSTEM: Windows 3.1
 ; SOFTWARE: WORD PERFECT 6.1 and ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/061,768A
 ; FILING DATE: APRIL 16, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA: NONE
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ARLES A. TAYLOR, JR.

; REGISTRATION NUMBER: 39,395
 ; REFERENCE/DOCKET NUMBER: 1242/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 493-8000
 ; TELEFAX: (919) 419-0383
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 677 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-09-061-768A-4
 ; Query Match 11.9%; Score 537.5; DB 3; Length 677;
 ; Best Local Similarity 25.6%; Pred. No. 1.6e-42; Indels 195; Gaps 30;
 ; Matches 205; Conservative 110; Mismatches 290;
 ; QY 89 AAGESAFRVTFDWD-----DEEFGVPGAFIKNLHFSBFFFLKSLTLEDVPHNG 136
 ; Db 47 AGAEDFEVTLPODVGTVMRLVHKAPPEVSLP-----LMSFSDAFCWFLEWLP-G 101
 ; QY 137 KVHFVCSNWPYANK--YKSRIFFPANQAYLPSETPTDLTKYRENELVTLRGDGTK--L 192
 ; Db 102 ALHFPYQWLEGAGELVLRGAAGVSWQDHP-----TLQDQKELSRQKWSWKTYI 156
 ; QY 193 EMDRVYDYAYNDLGDGDKGDLSPVLGSGSEYPPRRGTGRKPTKTDPNSESRIPL 252
 ; Db 157 EGWPRCLDHETVKDL-----DL----- 173
 ; QY 253 LMSLDIYVPRDRFGRHKLISDPLTALKSIVOLLPEFKALPDSHNEFDSFEDVLKYE 312
 ; Db 174 -----NIKYS-----AMKN-----AKLFFKAHSAYTELK----- 197
 ; QY 313 GGKILPOGSLKAITDSIPL-EILKELRSDEGLFKYPTPOVEDKTAWRTDEEFGRE 371
 ; Db 198 -----VKGLLDRGTGLWRLSREMR-----LFNFRKTPAAVYVFAHWQEDAFASQ 242
 ; QY 372 MLAGVNPVILSRLOEFPKSKLDPKIYQNSITITREQIEDKL-DGLTIDEAKTNRLFI 430
 ; Db 243 FLNGINPVLIRCHSLP-----NNPFVDEWVAPVLGPGTSLQAELEKGSFL 290
 ; QY 431 LNHHDILMPYLRRINTSTDTKTYASRTILFLQD-NGTLKPSAIEL-SLPHPDGOFGAVS 488
 ; Db 291 VD-HGILSGVHTNILNGKQPSAAWMTLLHQSSGSGPLLPINAIQLKQTFGPD-----N 342
 ; QY 489 KYVTPADQGVGSIWOLAKAYAANDSVGHQILSHLNTAAIEPFIATNRQLSALHPI 548
 ; Db 343 PIFLPSDDTDW---WLLAKTVVRNSEFVIEHVAVTHLHAHLIPEVFALATLRLPRCHPL 399
 ; QY 549 YKLLHPHRETMNINALARQILINGGGLLELV-----FPKYSMEKSAVVYKDWVFE 602
 ; Db 400 FKLLPHIRYTHINTLARELLVAPFKLIDKSTGLTGTFGLIKRNMELQNS-----V 454
 ; QY 603 QALPTDLIKRGVAVEDSSSPLGIRLLIQDYPAVDGLKIWSAKSWVTEYCNYYKSDDA 662
 ; Db 455 LCLPDIRARG--VED-----IFGYRDDGMQIWAIGAKSFVSEIYIYPSDTS 502
 ; QY 663 VOKDTLOAWKELREEGDKDKDPWPKMTVOELIDSCITITWIASALHAAVNFQY 722
 ; Db 503 VQDQELQAWVREIFSEGLGRESMPSLDREALVQYITMTVITCSAKHAAVSSGQF 562
 ; QY 723 PYAGVLPNRPILSRNFMPEPGSPYEELKTNPKVFLKTTITPOLQTLGISLIEILSRHS 782
 ; Db 563 DSCVMPNLPPTMQ--LPPPTS---KQARPEF-FIATLPVNSSSYHIIALWLLSABP 615
 ; QY 783 SDTLYIGORESPEWTKDQEPKLSAFARFGKLSLIEDQIMQNVDEKKNRSGPVKVPYTL 842
 ; Db 616 GDORPLGHYPDEHFTED-APRSVAAFORKLIQISKGI-----RERNGLALPTY 665
 ; QY 843 LPFTSEGLTGKIPNSVSI 862
 ; Db 666 LDPLP-----IENSVSI 677

RESULT 15

US-09-764-246-4
; Sequence 4, Application US/09764246
; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/764,246
FILING DATE: 17-Jan-2001

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 493-8000

TELEFAX: (919) 419-0383

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 677 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-764-246-4

Query Match 11.9%; Score 537.5; DB 4; Length 677;
Best Local Similarity 25.6%; Pred. No. 1.6e-42;
Matches 205; Conservative 110; Mismatches 290; Indels 195; Gaps 30;
QY 89 AAGESAFRTFDWD-----DEEFGVPGAFIKNLHFSFEFLKSLTLEDVPHNG 136
Db 47 AGAEEDEFVTLPODVGTVMLRVKAPPEVSLP-----LMSFRSDAWFCRWFELEWLPG-A 101
QY 137 KVHFVNSWYYPANK--YKSDRIFANQAYLPSETPDILKYRENELVTLRGDGTGK--L 192
Db 102 ALHFFCYQWLEGAGELVLRREGAAKWSQDHP-----TLQDQOKELESRKQWYSWKTYI 156
QY 193 EWDRVYDYAYNDLGDGDPKQDLSRPVLGGSSSEYPYRRGRTGRKPTKTDNSESRIPL 252
Db 157 EGWPRCLDHEVTKDL-----DL----- 173
QY 253 LMSLDIYVPRDRFRGHKLSDFLTALKSIVOLLPEFKALPDSSTHNEFDSFEDVLKLYE 312
Db 174 -----NIKYS-----AMKN-----AKLFFKAHSAYTELK----- 197
QY 313 GGKILPQGPILLKAITDSIPL--EILKELLRSDEGLFKYPTPQVIOEDKTAWRTDEFGRE 371
Db 198 -----VKGLLDRTGLMFLSREMR-----LFNFKKTPAAEYVFAHWQEDAFFASQ 242
QY 372 MLAGVNPVIISRLQEPFPKSLDKPIYGNQNSTITREQIEDKL-DGLTIDEAIKTNRLFI 430

Db 243 FLNGINPVLIRRRCHSLP-----NNFPVTDWVAPVLGPGTSLQAELEKSGSLFL 290
QY 431 LNHHDILMPYLRRINTSTDTKYASRTLLFLQD-NGTLKPSAIEL-SLPHPDQDFGAVS 488
Db 291 VD-HGILSGVHTNINLNGKPOFSAPMTLLHQSSGSGPLLPATQIKOTPGPD-----N 342
QY 489 KVVTPADOGVEGSIWOLAKAYAAVNDSGVHQLISHWLNTHAAIBPFVIATNRQLSALHPI 548
Db 343 PIFLPSDDTWD---WLLAKTWVRNSEFYIHEAVTHLLHAHLIPVFALATURQPRCHPL 399
QY 549 YKLIHPHFRETMINALARQILINGGELLETV-----FPKYSMEMSAYVYKDWVPPE 602
Db 400 FKLLIPIHRYTLHINTLARELLVAPGLDKSTGLGTGGFSDLIKRNMEQLNYS-----V 454
QY 603 QALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIAKSWTEYCNYIYKSDDA 662
Db 455 LCLPEDIRARG--VED-----IPGYVYRDDGMQIINGAIAKSFVSEIYIYPSDTS 502
QY 663 VOKDTLQAWKELRERGHGDKDEPWPKMOTVQOELIDSCITITWIASALHAAVNFQY 722
Db 503 VQDQELQAWVREIFSEFGLGRESGMPSLDITREALVQYITWVITCSAKHAAVSSGQF 562
QY 723 PYAGYLPNRPTLSRNFPEPGSPPEYELKTNPKVFLKTIIPQLQTLGLISLILSRHS 782
Db 563 DSCVMMENLPPTMQ--LPPPTS-----KGOARPEP-FIATLPVNSSSYHIIALWLSAEP 615
QY 783 SDTYLQGRESPEWTKDOEPLSAFARFGKLSLDTEDQIMQNVDEKWNKNSGPKVPVPTL 842
Db 616 GDQRPLGHYPDEHFTD-APRRSVAAPFORKLIQISKGI-----RERNRGLALPYTY 665
QY 843 LFPTSEGLTGKGIPINSVSI 862
Db 666 LDPLP-----IENSVSI 677

Search completed: March 10, 2005, 19:03:44

Job time : 50 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 13, 2005, 23:06:59 ; Search time 9293 Seconds
(without alignments)

4494.608 Million cell updates/sec

Title: US-10-731-642A-1

Perfect score: 4534

Sequence: 1 MFLEKIVDAITGDKDGKKV.....LFPTSEGGLTGKIPNSVSI 862

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xih
-Q=/cgn2_1/USPTO_spool/US10731642/runat_10032005_102235_5460/app_query.fasta_1.1031
-DB=GenEmbl -QMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10731642_CGN_1_1_5585 @runat_10032005_102235_5460 -NCPU=6 -ICPU=3
-NO_MMMap -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4534	100.0	2888	8	NTRNALOX1
2	4534	100.0	3390	6	AX644612 Sequence
3	4095	90.3	2915	8	AY008278 Lycopersi
4	3934	86.8	2831	8	STU60202 Solanum tub

5	3819.5	84.2	2740	8	AY254346
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13	3634.5	80.2	2818	8	AF019614
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17	3625.5	80.0	2851	8	LEU13681
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36	3066.5	67.6	2271	8	STLIPOXT13
37	3054	67.4	2562	8	ATH302043
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42	2911	64.2	2964	8	CSLBLOX
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ALIGNMENTS

RESULT 1	NTRNALOX1	N.tabacum mRNA for lipoxigenase.	2888 bp	linear	PLN 21-MAY-1998
LOCUS	X84040				
DEFINITION	X84040.1	GI:899343			
ACCESSION	X84040				
VERSION	X84040.1	GI:899343			
KEYWORDS	lipoxigenase; Lox1 gene.				
SOURCE	Nicotiana tabacum				
ORGANISM	Nicotiana tabacum				
REFERENCE	1	Veronesi, C., Fournier, J., Rickauer, M., Marolda, M. and Esquerre-Tugaye, M.T.			
AUTHORS	1	Veronesi, C., Fournier, J., Rickauer, M., Marolda, M. and Esquerre-Tugaye, M.T.			
TITLE	2	Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA (PGR95-009)			
JOURNAL	Plant Physiol.	108, 1342-1342 (1995)			
REFERENCE	2	(bases 1 to 2888)			
AUTHORS	Esquerre-Tugaye, M.T.				
TITLE	Direct Submission				
JOURNAL	Submitted (24-JAN-1995)	M.T. Esquerre-Tugaye, Universite Paul Sabatier, URA 1941 CNRS, Centre de Biologie et Physiol. Vegetales, 118 route de Narbonne, 31062 Toulouse, FRANCE			
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VERSION AY008278.1 GI:10764844
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Lycopersicon esculentum
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1 (bases 1 to 2915)
REFERENCE
AUTHORS Pan, Z., Feng, Q., Gilchrist, D.G. and Bostock, R.M.
TITLE Cloning and characterization of a toxin-induced lipoxigenase gene
in tomato
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 2915)
AUTHORS Pan, Z., Feng, Q., Gilchrist, D.G. and Bostock, R.M.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2000) Plant Pathology, University of California,
One Shields Ave., Davis, CA 95616, USA
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US-10-731-642A-1 (1-862) x AY008278 (1-2915)

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RESULT 4
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LOCUS Solanum tuberosum lipoxigenase (POTLX-3) mRNA, complete cds.
DEFINITION
ACCESSION U60202
VERSION U60202.1 GI:1407704
KEYWORDS
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamnids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 2831)
Kohliwats,M.V., Hannapel,D.J. and Gladon,R.J.
Nucleotide Sequence of a cDNA Clone for a Lipoxigenase from
Abscisic Acid-Treated Potato Leaves (Accession No.
U60202) (PGR96-069)
JOURNAL Plant Physiol. 112, 446 (1996)
REFERENCE
2 (bases 1 to 2831)
Kohliwats,M.V. and Hannapel,D.J.
Direct Submission
JOURNAL Submitted (07-JUN-1996) Horticulture, Iowa State University, Ames,
IA 50011, USA
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Gene

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39. 2627

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ORIGIN

Alignment Scores:

Pred. No.: 8.61e-307 Length: 2831
Score: 3934.00 Matches: 735
Percent Similarity: 92.48% Conservative: 64
Best Local Similarity: 85.07% Mismatches: 61
Query Match: 86.77% Indels: 4
DB: 8 Gaps: 3

US-10-731-642A-1 (1-862) x STU60202 (1-2831)

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1 (bases 1 to 2740)
REFERENCE
AUTHORS Halitschke, R. and Baldwin, I.T.
TITLE Antisense LOX expression increases herbivore performance by
decreasing defense responses and inhibiting growth-related
transcriptional reorganization in Nicotiana attenuata
Plant J. 36 (6), 794-807 (2003)
JOURNAL
PUBMED 14675445
2 (bases 1 to 2740)
REFERENCE
AUTHORS Halitschke, R. and Baldwin, I.T.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2003) Molecular Ecology, Max Planck Institute for
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FEATURES
source
1 (bases 1 to 2832)
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Halitschke, R. and Baldwin, I.T.
Antisense LOX expression increases herbivore performance by
decreasing defense responses and inhibiting growth-related
transcriptional reorganization in Nicotiana attenuata
Plant J. 36 (6), 794-807 (2003)
14675445
Halitschke, R. and Baldwin, I.T.
Direct Submission
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REFERENCE 1 (Bases 1 to 2718)  
AUTHORS Geerts,A., Feltkamp,D. and Rosahl,S.  
TITLE Expression of lipoygenase in wounded tubers of Solanum tuberosum L  
JOURNAL Plant Physiol. 105 (1), 269-277 (1994)  
MEDLINE 94302170  
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Qy 130 GluAspValProAsnHisGlyLysValHisPheValCysAsnSerTrpValTrpProAla 149
Db 378 GAAGATGTCCTATCATCGGCAAGTCCATTTTGTTCGAATTTCTTGGTTTATCCATCT 437
Qy 150 AsnLysTrpLysSerAspArgIlePhePheAlaAsnGlnAlaTrpLeuProSerGluThr 169
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DEFINITION Solanum tuberosum lipoxigenase (POTLX-2) mRNA, complete cds.
ACCESSION U60201
VERSION   U60201.1 GI:1407702
KEYWORDS .
SOURCE   Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2837)
Kolomiets, M.V., Hannapel, D.J. and Gladon, R.J.
Potato Lipoxigenase Genes Expressed During the Early Stages of
Tuberization (Accession Nos. U60200 and U60201) (PGR96-065)
2 (bases 1 to 2837)
Kolomiets, M.V. and Hannapel, D.J.
Direct Submission
Submitted (07-JUN-1996) Horticulture, Iowa State University, Ames,
IA 50011, USA
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Alignment Scores:
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QY      100 AspTrpAspAspGluGluPheGlyValProGlyAlaPheIlelleLysAsnLeuHisPhe 119
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QY      120 SerGluPheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHis 139
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QY      140 PheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePhe 159
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QY      180 GluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTyrAspArgValTyr 199
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DB      821 GTACCAAGAGATGAGCGTTTGGTCACTTGAAGATGTCCAGACTTCTTAACATATGCTTTG 880

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DEFINITION U09026
ACCESSION U09026.1 GI:575432
VERSION U09026.1
KEYWORDS Lycopersicon esculentum (tomato)
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 2842)
AUTHORS Ferrie,B.J., Beaudoin,N., Burkhardt,W., Bowsher,C.G. and
Rothstein,S.J.
TITLE The cloning of two tomato lipoxygenase genes and their differential
expression during fruit ripening
JOURNAL Plant Physiol. 106 (1), 109-118 (1994)
MEDLINE 95062736
PUBMED 7972514
REFERENCE 2 (bases 1 to 2842)
AUTHORS Ferrie,B.J.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1994) Bonita J. Ferrie, University of Guelph,
Molecular Biology and Genetics, Guelph, Ontario, N1G 2W1, Canada
COMMENT On Nov 28, 1994 this sequence version replaced gi:482902.
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 ACCESSION Y18548
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 ORGANISM Solanum tuberosum
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 asterids; lamids; Solanales; Solanaceae; Solanum.
 1 Hughes, R.K., West, S.I., Hornostaj, A.R., Lawson, D.M.,
 Fairhurst, S.A., Sanchez, R.O., Hough, P., Robinson, B.H. and Casey, R.
 Probing a novel potato lipoxigenase with dual positional
 specificity reveals primary determinants of substrate binding and
 requirements for a surface hydrophobic loop and has implications
 for the role of lipoxigenases in tubers
 Biochem. J. 353 (Pt 2), 345-355 (2001)
 JOURNAL Biochem. J. 353 (Pt 2), 345-355 (2001)
 MEDLINE 21056065
 PUBMED 11139400
 REFERENCE 2 (bases 1 to 2818)
 AUTHORS Casey, R.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1998) R. Casey, John Innes Institute, Colney
 Lane, Norwich NR4 7UH, UK
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ORIGIN

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 ACCESSION AF019614
 VERSION AF019614.1 GI:2558850
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 SOURCE Solanum tuberosum
 ORGANISM Solanum tuberosum
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE 1 (bases 1 to 2818)
 AUTHORS Fidansef,A.L. and Bostock,R.M.
 TITLE Solanum tuberosum (Lehmi Russet) lipoxigenase (plox2) mRNA,
 complete cds
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2818)
 AUTHORS Fidansef,A.L. and Bostock,R.M.
 TITLE Direct Submission
 JOURNAL Submitted (14-AUG-1997) Plant Pathology Department, University of
 California, Davis, One Shields Avenue, Davis, CA 95616, USA
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Best Local Similarity: 78.8% Mismatches: 92
Query Match: 80.1% Indels: 3
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US-10-731-642A-1 (1-862) x AF019614 (1-2818)

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RESULT 14

AF039651

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

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Query Match:

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US-10-731-642A-1 (1-862) x AF039651 (1-2843)

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1 (bases 1 to 2843)

Chen, X., Reddanna, P., Reddy, G.R., Kidd, R., Hildenbrandt, G. and Reddy, C.C.

Expression, purification, and characterization of a recombinant 5-lipoxygenase from potato tuber

Biochem. Biophys. Res. Commun. 243 (2), 438-443 (1998)

98153783

9480827

2 (bases 1 to 2843)

Chen, X., Reddanna, P., Reddy, G.R., Kidd, R., Hildenbrandt, G. and Reddy, C.C.

Direct Submission

Submitted (22-DEC-1997) Veterinary Science, Pennsylvania State University, 226 Fenske, University Park, PA 16802, USA

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1.4e-282

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Matches: 674

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Conservative: 83

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Mismatch: 92

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Indels: 3

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Gaps: 3

US-10-731-642A-1 (1-862) x AF039651 (1-2843)

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 ACCESSION X79107
 VERSION 95175602
 KEYWORDS lipoxigenase.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE

1 Casey, R.

Sequence of a cDNA clone encoding a potato (Solanum tuberosum)

AUTHORS

TITLE

tuber lipoxigenase

JOURNAL

Plant Physiol. 107 (1), 265-266 (1995)

MEDLINE

95175602

PUBMED

7870815

REFERENCE

2 (bases 1 to 2809)

AUTHORS

Casey, R.

Direct Submission

Submitted (09-MAY-1994) R. Casey, John Innes Institute, Colney

Lane, Norwich NR4 7UH, UK

JOURNAL

TITLE

Location/Qualifiers

FEATURES

source

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NSVSI"

ORIGIN

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Score: 3632.50 Matches: 672

Percent Similarity: 88.62% Conservative: 83

Best Local Similarity: 78.87% Mismatches: 94

Query Match: 80.12% Indels: 3
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Job time : 9404 secs

GenCore version 5.1.1.6
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(without alignments)
4493.979 Million cell updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3202.5	70.6	2580	9	US-09-938-842A-1504
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ALIGNMENTS

RESULT 1
US-10-731-642A-2
; Sequence 2, Application US/10731642A
; Publication No. US20040205942A1
; GENERAL INFORMATION:
; APPLICANT: MENE-SAFFRANE, Laurent
; APPLICANT: ESQUERRE-TUGAYE, Marie-Therese
; APPLICANT: FOURNIER, Joelle
; APPLICANT: BEFFA, Roland
; APPLICANT: GROSJEAN-COURNOVER Marie-Claire
; TITLE OF INVENTION: LIPOXYGENASE OVEREXPRESSION IN PLANTS
; TITLE OF INVENTION: AND REDUCTION IN PLANT SENSITIVITY TO
; TITLE OF INVENTION: DISEASES AND TO ATTACKS FROM PATHOGENIC
; TITLE OF INVENTION: ORGANISMS
; FILE REFERENCE: A36097-PCT-USA-A 075188.0117
; CURRENT APPLICATION NUMBER: US/10/731,642A
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/FR02/01943
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: FR 01/07470

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; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: FR 01/14358
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Custom
; SEQ ID NO 2
; LENGTH: 3390
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: construct CamV 35S-LOX
; NAME/KEY: promoter
; LOCATION: (1)..(532)
; OTHER INFORMATION: CamV 35S promoter
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (543)..(3131)
; OTHER INFORMATION: Tobacco LOX1 coding sequence
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3138)..(3390)
; OTHER INFORMATION: Nos terminator
US-10-731-642A-2

Alignment Scores:
Pred. No.: 0 Length: 3390
Score: 4534.00 Matches: 862
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-731-642A-1 (1-862) x US-10-731-642A-2 (1-3390)

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Db 543 ATGTTCTGGAGAGATTGTGGATGCATCACAGGAAAGATGAGGAAAGGTAAAA 602
Qy 21 GlyThrValValLeuMetLysLysValLeuAspPheThrAspIleAsnAlaSerVal 40
Db 603 GCAACAGTGGTTTTCATGAAGAAAAATGTTTGGATTTTACTGATATTAATGCCTCAGTT 662
Qy 41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerSerVal 60
Db 663 CTGTGATGAGTTCTTGAGTTCTTGGTGGAGGGTCTCTCTGAGTTGATCAGTTCTGTT 722
Qy 61 AsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrlLeuGluAsn 80
Db 723 AATGCTGATCTGCAATGGTTTACAGGGAACCCAGCAAGCAGCATATTTGGAGAAC 782
Qy 81 TrpLeuThrAsnSerThrProIleAlaAlaGlyLysAlaPheArgValThrPheAsp 100
Db 783 TGGCTTAACAAATAGCACCCCAATAGCAGCAGTGAATCAGCATTTAGAGTCACATTTGAT 842
Qy 101 TrpAspAspGluPheGlyValProGlyAlaPheIleLysAsnLysHisPheSer 120
Db 843 TGGGATGATGAGGAATTTGGAGTTCCAGAGCAATTCATTTACAGAACTTCGATTTTAGT 902
Qy 121 GluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPhe 140
Db 903 GAGTTCTTCCCACTCACTACCCTTGAAGATGTTCTCTATCATGCGCAAGTTTCATTTT 962
Qy 141 ValCysAsnSerTrpValTyrlProAlaLysTyrlLysSerAspArgIlePhePheAla 160
Db 963 GTCTGAATTTCTTGGGTTTATCCTGCTAATAAATATAAGTCAGATCGCATCTTCTTCGCG 1022
Qy 161 AsnGlnAlaTyrlLeuProSerGluThrProAspThrLeuArgLysTyrlArgGluAsnGlu 180
Db 1023 AATCAGGCTTATCTACCAAGTGAACCCAGACACATTCGCGAAATACAGAGAAATGAA 1082
Qy 181 LeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTyrlPheAspArgValTyrlAsp 200
Db 2163 CAACTAAGCGGCTTCAACCTATTATAAGCTTCTCCACCCCTCATTTCCGTCGAGACGATG 2222
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1083 TTACTAACCTTAAGAGGAGATGGAACCTGGAAGCTTGAGGAATGGATAGAGTTTATGAC 1142

201 TyrAlaTyrlTrpAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProVal 220

1143 TATGCTTACTACATGATTTGGGTGATCCAGACAAAGCCCAAGATTTGTCAAGSCCTGTC 1202

221 LeuGlyGlySerSerGluTyrlProTyrlProArgArgGlyArgThrGlyArgLysProThr 240

1203 TTAGGAGATCTTCTGATACCTGATCCGTTATCTCTAGAGGAGGACAGGCGCCAAACCAACC 1262

241 LysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrlVal 260

1263 AAAACAGATCTTAATCCGAGAGCAGGATTCATTTGCTTATGAGCTTAGACATATATGTG 1322

261 ProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLys 280

1323 CCAAGGAGCAGGCGATTTGGTCATATAAGTTGTCAGACTTCTTGACATTTGCTTTGAAA 1382

281 SerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGlu 300

1383 TCCATTTGTGAGTTGCTTCTCCCTGAGTTTAAGGCTTTGTCGATAGCACCATATAGAG 1442

301 PheAspSerPheGluAspValLeuLysLeuTyrlGluGlyGlyIleLysLeuProGlnGly 320

1443 TTTGATAGTTTGGAGGATGACTTAAACTGTATGAAGGAGGAATCAAGTTGCCTCAAGGC 1502

321 ProLeuLysAlaIleThrAspSerIleProLeuGluLysLysLysLysLysLysLys 340

1503 CCTTTGTGAAAGCCATTTACTGATAGCATTCCTTTAGAGATACATAAAGAACTCCTTCGA 1562

341 SerAspGlyGluGlyLeuPheLysTyrlProGlnValIleGlnGlnAspLysThr 360

1563 AGTGATGGTGAAGGCTTATTTAAGTACCAACTCTCAGGTTTATCAAGAGGATATAAACT 1622

361 AlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIle 380

1623 GCATGGAGGAGCGGATGAAGAAATTTGGGAGAGAAATTTGGCGGAGTCAATCTCTGTATA 1682

381 IleSerArgLeuGlnGluPheProLysSerLysLysLysLysLysLysLysLysLys 400

1683 ATCAGTAGACTCCAGAAATTCCTCCGAAAGAGAAAGTTGGATCCTTAAATAATATATGGCAAC 1742

401 GlnAsnSerThrIleThrArgGluGlnIleLysLysLysLysLysLysLysLysLys 420

1743 CAAAACAGTACAATTAACAGAGACAGATAGAGATTAAGTTGGATGGACTTAACATTCAT 1802

421 GluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrl 440

1803 GAGCAATCAAGACTAAGACACTATTCATATTTGAACCATCATGATATCTTTATGCCATAC 1862

441 LeuArgArgIleAsnThrSerThrAspThrLysThrTyrlAlaSerArgThrIleLeuPhe 460

1863 TTGAGGAGAAATTAACAGTCGACAGACACAAACCTTATGCTTCAAGAACTCTGCTCTTC 1922

461 LeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAsp 480

1923 TTGCAAGATTAAGAACTTTGAAGCCATCAGCAATTAAGCTTAAGCTTGCACATCCAGAC 1982

481 GlyAspGlnPheGlyAlaValSerLysValTyrlThrProAlaAspGlnGlyValGluGly 500

1983 GGAGATCAATTTGGCGCTTTAGCAAAAGTATATACACCAGCTGATCAAGGTTGTTGAAGGT 2042

501 SerIleTrpGlnLeuAlaLysAlaTyrlAlaValAsnAspSerGlyValHisGlnLeu 520

2043 TCTATCTGGCAGTTGGCCAAAGCCCTATGACAGTGAATGATTCGGCGGTTTCATCACTC 2102

521 IleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArg 540

2103 ATCAGTCACTGGTTGAATACATGACGAGCATAGAGCAATTCGTGATCGCAACAAATAGG 2162

541 GlnLeuSerAlaLeuHisProIleTyrlLysLeuLeuHisProHisPheArgGluThrMet 560

2163 CAACTAAGCGGCTTCAACCTATTATAAGCTTCTCCACCCCTCATTTCCGTCGAGACGATG 2222

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561 AsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThr 580
2223 AACATAAATGCTTACAGACAGATCTTGATCAACGGTGGGACTCTTGGATTGACA 2282
581 ValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhe 600
2283 GTTTTTCCGCCCAATATTCATGGAATGTACAGCAGTAGTTTACAAAGACTGGGTTTC 2342
601 ProGluGlnAlaLeuProThrAspIleLysArgGlyValAlaValGluAspSerSer 620
2343 CTGACCAAGACACTTCTACTGATCTCATCAAAAGAGAGTAGTCTGTGAGGACTCGAC 2402
621 SerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLys 640
2403 TCCCACTTGGCATTCGATTACTGATTCAGGACTATCCATATGCTGTGATGGTTGAAA 2462
641 IleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAsp 660
2463 ATTGGTCAGCAATTAAGAGTTGGGTAACTGAATACCTGCAACTACTATTACAAATCAGAT 2522
661 AspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGly 680
2523 GATCGGGTTCAAAAGACACTGAACCTCAAGCCTGGTGGAAAGAACTCCGCGAAGAGGA 2582
681 HisGlyAspLysLysAspGluProTyrTrpProLysMetGlnThrValGlnGluLeuIle 700
2583 CACGGTGACAGAGAGATGAGCTTGGTGCCCTAAATGCACACAGCTGCAAGATTGATA 2642
701 AspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHiAlaAlaValAsnPheGly 720
2643 GACTCTTGCAACCATCAATATGATAGTCTTCAGCACTTCATGCAGCAGTCAATTTGGG 2702
721 GlnTyrProTyrAlaGlyTyrIleuProAsnArgProThrLeuSerArgAsnPheMetPro 740
2703 CAATACCTCTATGCTGGTTATCTCCCTAATCGCCCTACATTAAGCGCAATTTTCATGCCA 2762
741 GluProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLys 760
2763 GAGCCAGGAGTCTGAGTATGAGAGCTCAAGACAAATCCGGATAGTATTCCTCANA 2822
761 ThrIleThrProGlnLeuThrLeuLeuGlyIleSerLeuIleGluLeuSerArg 780
2823 ACAATCACTCTCTCAGCTGCAGACACTGCTTGGCATTTCCCTCATAGAGATCTTGTCAAG 2882
781 HisSerSerAspThrLeuTyrIleuGlyGlnArgGluSerProGluTyrTrpLysAspGln 800
2883 CATCTCTCGGATACACTTTTACCTCGGGCAAGGGAATCACCTGAATGGCAAAAGGATCAA 2942
801 GluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIle 820
2943 GNAACACTTTTACGCTTTTCCGAGGTTTGGAAAGAGCTGAGTGATATCAGGATCAGATT 3002
821 MetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyr 840
3003 ATGCAGATGAATGTCGATGAGAAATGGAAGACAGCTCGGGTCTCTGTAAAGTTCCATAC 3062
841 ThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerVal 860
3063 ACCTTGCTCTTCCCAACAGTGAAGAGGAGACTTACTGGCAAGGAATTCCTAACAGTGTG 3122
861 SerIle 862
3123 TCAATA 3128

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RESULT 2

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US-10-425-114-12761
; Sequence 12761, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

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; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12761
; LENGTH: 2744
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701209742_FLI
US-10-425-114-12761

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Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Mismatches:	Indels:	Gaps:
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Percent Similarity:	84.46%					
Best Local Similarity:	70.20%					
Query Match:	73.81%					
DB:	17					

US-10-731-642A-1 (1-862) x US-10-425-114-12761 (1-2744)

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QY 16 GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp 35
Db 136 GGGCACCCAGGTGAAAGGACGGTGTGTGTGATGAAGAAATGTGTGTGACTTCAACGAT 185
QY 36 IleAsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyValArgValSerLeuGlu 55
Db 186 TTCAGTGTCTCGTTCTTTCATGCTCTTCATGAGTTTGTGGGAAACGAGTTCTCTTCAG 245
QY 56 LeuIleSerSerValAsnAlaAspPro-----AlaAsnGlyLeuGlnGlyLysArgSer 73
Db 246 CTCGTAACTTCTGTCAACGTTGACCTGGGAATGGCAATGGGTTGAAGGGGAAACTTGGG 305
QY 74 LysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSer 93
Db 306 AGCCTGCTTATCTAGAAGACTGGATCACAAATAGCACCTTTGACAGCAGGAGAACCA 365
QY 94 AlaPheArgValThrPheAspTrpAspGluGluPheGlyValProGlyAlaPheIle 113
Db 366 GCATTCAGGTCACATTTGAGTGG---GATGAGGAGATAGGAACACACGAGGACATTATA 422
QY 114 IleLysAsnLeuHisPheSerGluPheLeuLysSerLeuThrLeuGluAspValPro 133
Db 423 ATAAGGAACAATCATCATAGTGTGAGTTCTACCTCAAAAGCCTGACACTAGAAGATGTCCA 482
QY 134 AsnHisGlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLys 153
Db 483 GGCCAAAGTGTCACTTCGCTTTATCTGCAACTCTTGGGTATACCCCTGCTGATAAATATGAA 542
QY 154 SerAspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeu 173
Db 543 AAGGATCGCATTTCTTCTCCCAACAGACATACCTTCCCAAGTGAACACCAATGCCACTA 602
QY 174 ArgLysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGlu 193
Db 603 CTTAAGTACAGAGAAGAGAGTTGAGAAATTTAAGAGGTAATGGGAGGGTCAGCTCCAA 662
QY 194 GluTrpAspArgValTyrAspTyrAlaTyrTrpAsnAspLeuGlyAspProAspLysGly 213
Db 663 GAGTGGGACAGGGTCTATGATTATGCTCTCTACAAATGATTTGGGAAATCCCGATTAAGGT 722
QY 214 GlnAspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGly 233

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Db 723 CCACAAATGCTCGTCTACTCTAGGAGGCTTAAGGATTACCCCTCCCTAGGGGA 782
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Db 783 AGAACTAGTAGACCAACCGCCCAAAATCAGATCTCTAAATGTGAGAGTAGGCTGAATATTGCC 842
Qy 254 MetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLeuLeuSerAsp 273
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Qy 274 PheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeu 293
Db 903 TTTCTTGCTATGCACTGAAATCCATAGTCAAGTTCTCAAAACCGGAGTTTGAATCTCTA 962
Qy 294 PheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGly 313
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Qy 314 GlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGlu 333
Db 1023 GGGATTGAGGTGCTCGAGGT---ATCTTACGGAAGTTAGGATTAACATCTCTGCAGAG 1079
Qy 334 IleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGln 353
Db 1080 ATGCTTAAAGGAATTTCCGATCTCAGCGGCAAGGCTTCTCAAAATTTCCGTCGCTCAA 1139
Qy 354 ValIleGlnGluAspLysThrAlaTyrArgThrAspGluGluPheGlyArgGluMetLeu 373
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Qy 374 AlaGlyValAsnProValIleLeuSerArgLeuGlnGluPheProProLysSerLysLeu 393
Db 1200 GCTGTATAAACCCCTGTTGTAATTCGTGTCCTCAAGAGTTCCCAACAGCAAGCACTA 1259
Qy 394 AspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLys 413
Db 1260 GATCCCAAAATCTACGGTAATCAAACTAGCACAAATAACCAAGAACACATCGAAAGTAAC 1319
Qy 414 LeuAspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHis 433
Db 1320 CTGGAAGGTTCCACAGTAGATGAGCAATTAAGAAAGAGGTTGTTTCATTTAGATCTC 1379
Qy 434 HisAspIleLeuMetProTyrLeuArgIleAsnThrSerThrAspThrLysThrTyr 453
Db 1380 CACGATGATGATACCATGCTGAGAGGATAAC---TCTACTTCTACAAAGATGAT 1436
Qy 454 AlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGlu 473
Db 1437 GCAAGCAGGACAAATCTGTTCTTCAAGATAGTGGGACTTTGAAGCCCACTAGCCATTGAG 1496
Qy 474 LeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrPro 493
Db 1497 TTGAGTTTGCCCTCATCTCTGAGGAGATCAATATGTTGCAATAAGTAAGTTTACACGCC 1556
Qy 494 AlaAspGlnGlyValGluGlySerIleTyrGlnLeuAlaLysAlaTyrAlaValAsn 513
Db 1557 GTGGACCAAGGCTTGAAGAACTCTCTTGGCAACTTGGCCAAAGCTTATGTAGTGTAGCT 1616
Qy 514 AspSerGlyValHisGlnLeuLysSerHisThrLeuAsnThrHisAlaAlaIleGluPro 533
Db 1617 GACTCAGGCTATCATCACTTATCAGCCACTGTTGTCATCTATCATGCACTTATGAGCCA 1676
Qy 534 PheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHis 553
Db 1677 ATTATTTAGCTTACAAATAGGACCTTATGTGCTTCCACCTTATTCATAAGCTATTGCA 1736
Qy 554 ProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuLysAsnGly 573
Db 1737 CTCTACTTCTGACACCATGATATAATATGCACTCGGACGACAGATCTCATTAATGCA 1796
Qy 574 GlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaVal 593
Db 1797 GGTGGTGTCTTAGAGTTAACAGTTTGTCATCTAAGTATCTATGAGGTTTTCATCTGTG 1856

Qy 594 ValTyrLysAspTyrValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGly 613
Db 1857 CTTTACAGGACTGGGTTTCCCTCGAGCAGCATGCTGAGACCTTGTCAAGAGAGA 1916
Qy 614 ValAlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrPro 633
Db 1917 GTGGCTGTTAAGGACTCAACTTCCCGCTATGGCTTCGATTATTGATTGAGGATTACCT 1976
Qy 634 TyrAlaValAspGlyLeuLysIleTyrSerAlaIleLysSerTyrValThrGluTyrCys 653
Db 1977 TTTTCAGTTGATGGCTAGAGATTGTTGCTATCAAAACATGGGTTAAGGACTACTGC 2036
Qy 654 AsnTyrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTyrTyr 673
Db 2037 TCCCTTTACTACAAGGAGGATGACACTATCAAGAAAGATCTGAACCTTCAATCTTGGTGG 2096
Qy 674 LysGluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTyrTyrProLysMet 693
Db 2097 AAGCAATAAGGAGGTGGTTCATGGTGACAAAGATGAGCCTTGTGGCCAAAGATG 2156
Qy 694 GlnThrValGlnGluLeuIleAspSerCysThrIleThrIleThrIleAlaSerAlaLeu 713
Db 2157 CAGACATGTGAAGAGCTGATTTCAGACTTGCATATTATCATATGATGCTCCCTCAGCTCTC 2216
Qy 714 HisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThr 733
Db 2217 CATCTGCAATCAACTTTGGCAATATCCATATGGAGCTTCCACCGAGTGTCCGGCT 2276
Qy 734 LeuSerArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsn 753
Db 2277 ATAAGCCGCGGATTCATGCCAGAAAGAAAGAACTCCAGAAATACGATGAACCTTGTGCGAAT 2336
Qy 754 ProAspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyLysSer 773
Db 2337 CCTGATAAGGCTTATCTGAAACACAGTTACTTTCACAGTTTCTGGCTGTCTTGGCATTTCA 2396
Qy 774 LeuIleGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSer 793
Db 2397 CTTGTAGAGATCTTGTCCAAACATTTAGTGATGAGGTCTACCTTGGCCAGAGACACT 2456
Qy 794 ProGluTyrThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeu 813
Db 2457 CCAGATTGGACATCTGATGCTGAGCCATTCAGACCTTTGAGAAAGTTTGGCAAAACCTT 2516
Qy 814 SerAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSer 833
Db 2517 GCTGATATTGAGGAAGGATCTTGAGATGAATAGTATGAGAAATTCAGAAACCGGTAT 2576
Qy 834 GlyProValLysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGly 853
Db 2577 GGTCCAGTTAAGATGCCCATACACCTTGTCTTATCTTCTAGTAAGGTGGACTAATCGC 2636
Qy 854 LysGlyIleProAsnSerValSerIle 862
Db 2637 ATGGGGTTCCTAACAGTATCTCAATT 2663

RESULT 3

US-09-978-522-4
; Sequence 4, Application US/09978522
; Publication No. US20030033627A1
; GENERAL INFORMATION:
; APPLICANT: Descenzo, Richard
; APPLICANT: Ireland, Nancy
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera
; FILE REFERENCE: 29520/37890
; CURRENT APPLICATION NUMBER: US/09/978,522
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,220
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4

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; ORGANISM: Vitis LOX sequence 2		Db		901	GGGCCACTGCGCAAGTACAGAGAAAGGGAACCTGGGAATCTGAGGGAGATGGAACCGGA	960
US-09-978-522-4		Qy		191	LysLeuGluGluTirAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspPro	210
Alignment Scores:		Db		961	GAGCTTAAGGAATGGATCGATGATGACTATGCTTACTATAATGATTTGGGAATCCA	1020
Pred. No.: 0		Qy		211	AspLysGlyGlnAspLeuSerArgProValLeuGlyLysSerSerGluTyrProTyrPro	230
Score: 3254.50		Db		1021	GACAGGATCTCAATACGCCGCCCTGTGCTGGGAGGATCTGCAGAGTATCTCTTATCCC	1080
Matches: 660		Qy		231	ArgArgGlyArgThrGlyArgLysProThrLys	241
Percent Similarity: 63.28%		Db		1081	AGGAGGGAAGAACTGGTAGACCACCATCTGAAAAAGGTAGATATTTGATGCAAAATTC	1140
Best Local Similarity: 54.59%		Qy		241	-----	241
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Indels: 35		Qy		242	-----ThrAspProAsnSerGluSerArgLysProLeuLeuMetSerLeuAspLys	259
Gaps: 10		Db		1201	TTAATTAACAGATCCCAACACCGAGAGAGATTTGCCACTTGTGATGAGCTTAAACATATA	1260
US-10-731-642A-1 (1-862) x US-09-978-522-4 (1-4237)		Qy		259	rValProArgAspGluArgPheGlyHisLysLeuSerSerAspPheLeuThrPheAlaLe	279
		Db		1261	TGTTTCAAGAGATGAAGATTTGGTCACTGAAGATGTCAGACTTCTTGGCTTATGCCCCT	1320
		Qy		279	uLysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAs	299
		Db		1321	GAAATCCATAGTTCAATTCCTTCTCCCTGAGTTTGGAGCTCTATGTGACATCACCACAA	1380
		Qy		299	nGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyLysLeuProGlu	319
		Db		1381	TCAGTTTGACAGCTTCCAGATGTATTAGACCTCTACGAAGAGGAATCAAGTCCACAGA	1440
		Qy		319	nGlyProLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeu	339
		Db		1441	GGGCCCTTTTACTGGCAAAATTAAGGACAACATCCCTCTTGAGATGCTCAAGGAATCTGT	1500
		Qy		339	uArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGln	356
		Db		1501	TCGTACTGATGGGAACATCTCTTCAAGTTCCTCAATGCCCAAGTCAATCAAGAGTACTGC	1560
		Qy		356	-----	356
		Db		1561	ATACATCTAAACATCTTGTAAATCTTTTGAAGCCAGATTTATATATTTTTCGTAAAAAT	1620
		Qy		357	-----GluAspLysThrAlaTirPargThrAspGluGluP	368
		Db		1621	GATGAGTTTTTATCATGCTGGAGCAGAGGATAAGTCTGTCATGGAGGACCGATGAAGAT	1680
		Qy		368	heGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArg	383
		Db		1681	TTGCAAGAGAATGCTGCTGGACTCAACCCAGTGTGTCATCG-TCTACTCCAGTAAC	1739
		Qy		383	-----	383
		Db		1740	TACAGCTTCTTCAATATATTTTAAATGCCCTGTTTGTGTTTCTGAGAAAAATGGAATTG	1799
		Qy		383	-----	383
		Db		1800	GAAAGGCTTCCAGACTTTGTTTCTTCCCTCCATCTACTGTTCTAGCTCTTTTCTGATA	1859
		Qy		384	-----LeuGlnGluPheProLysSerLysLeuAspProL	396
		Db		1860	ATTATTGCTTTTCTACTTTTGTGTCAGGAGTTTCTTCCAAAAAGCAAGCTGGATCTGT	1919
		Qy		396	ysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspG	416
		Db		1920	AAGTTTATGGCAACCAAAACAGTTTCAATAACCAAAAGAACACATAGAGAATTCACCTGGATG	1979

; LENGTH: 4237		Qy		22	3 LeuGluLysIleValAspAlaIleThrGlyLysAspAspGlyLysValLysGlyThr	22
; TYPE: DNA		Db		63	4 APTCAATCAATTTGTTGGTGCCATTACTGGCGAAATGATTAAGAAAGATCAAGGGAAC	63
; ORGANISM: Vitis LOX sequence 2		Qy		42	23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp	42
US-09-978-522-4		Db		123	64 GTTGTGTTGATGAAGAAGATGTGTTGATTTTATGACTTCAATGCATCGGTTCTGGAC	123
Alignment Scores:		Qy		62	43 GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuLysSerSerValAsnAla	62
Pred. No.: 0		Db		183	124 CGGGTTTCATGAGCTGTGGGACAGGAGTCCCTCTGCAGCTCGTCAGTGTCTTCATGCT	183
Score: 3254.50		Qy		64	63 AspPro-----	64
Matches: 660		Db		243	184 GATCCTGGTGAGTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	243
Percent Similarity: 63.28%		Qy		64	-----	64
Best Local Similarity: 54.59%		Db		303	244 GGGTTATTGAAGTTGGGGAGAGAGAGATGATGCGGTTTTGTGAGGGGTGAGATGGTT	303
Query Match: 71.78%		Qy		64	-----	64
Indels: 35		Db		363	304 TTGAGTTTTGATGATGGGAGTTGGAAGAAGATGTGTTTTTGGAGAAGGTCAAGAGGGT	363
Gaps: 10		Qy		64	-----	64
US-10-731-642A-1 (1-862) x US-09-978-522-4 (1-4237)		Db		423	364 TATTCTCAGAAATTGATGCAATGAGTTTCTTGACATCTTCCATTCAGCTGGGCACTTTTC	423
		Qy		67	65 -----AlaAsnGly	67
		Db		483	424 TAAGTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	483
		Qy		87	68 LeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSerThrPro	87
		Db		543	484 TTACAGGGGAAATTTGGAACCCAGCATACTTTGGAAGACTGGATTACCAATATCTTCT	543
		Qy		107	88 IleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAspAspGluGluPheGly	107
		Db		600	544 TTAACCGGGGGAGTCTGCAATTCAGGTTCAGCTTCGACTGG- -GATGAGGAGATTGGA	600
		Qy		127	108 ValProGlyAlaPheIleLysAsnLeuHisPheSerGluPhePheLysSerLeu	127
		Db		660	601 GAGCAGGGGCATTCATTAATTAGAACAATACACAGTGAGTTTACCTCAGGACTCTC	660
		Qy		147	128 ThrLeuGluAspValProAsnHisGlyLysValHisPheValCysAsnSerTrpValTyr	147
		Db		720	661 ACTCTTGAAGATGTTCTTGGAGCTGGCAGAAATTCATTTGTTGTTGTTGTTGTTGTTGTTG	720
		Qy		161	148 ProAlaAsnLysTyrLysSerAspArgLlePhePheAlaAsn-----	161
		Db		780	721 CCTGCTCAGCACTACAAAACGACCGTGTGTTTCTTCACTAATCAGTAAGACTAATTTAC	780
		Qy		161	-----	161
		Db		840	781 TTGATACTAGGAGATCTGCTGTGGATTTGTGGCTCATTTGAGCTTAGGCAAGGAAATG	840
		Qy		170	162 -----GlnAlaTyrLeuProSerGluThrPro	170

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QY 416 lyleuThrileAspGluAla----- 422
Db 1980 ACCTTTACTATAAACGAGGT-AACGCTCTTAGTGTCCCTCTTTCAGACTAAATTTTCAA 2038
QY 422 ----- 422
Db 2039 TGTGCACATGTTAATTTTTCATTTGCAATGGAACACACAGCCATAGTAACCTGAAATAATGGTGTCT 2098
QY 423 -----IleLysThrAsnArgLeuPheLleLeuAsnHisAspIleLeuMetp 439
Db 2099 TTTACTAGGCAATGAGAGAAGAGGCTATTATATAGATACCATGATGTTTTCATGC 2158
QY 439 roTyLeuArgAlaGlnThrSerThrAspThrLysThrTyAlaSerArgThrLeuL 459
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QY 459 euPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisP 479
Db 2216 TCTTCTGAAAGACGACGGAACCTTTGAAGCCACCTGGCGAATTGAATTGAGCCTACCAATC 2275
QY 479 roAspGlyAspGlnPheGlyAlaValSerLysValTyThrProAlaAspGlnGlyValG 499
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QY 499 luGlySerIleTrpGlnLeuAlaLysAlaTyAlaAlaValAsnAspSerGlyValHisG 519
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QY 519 lnLeuIleSerHisTrpLeu----- 525
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QY 526 -----AsnThrHisAlaLal 531
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QY 531 leGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyLysL 551
Db 2515 TTGAGCCATTTGTGATTTGCAACCAACAGCGAGCTCAGCGTCTTCATCCAATTCACAAGC 2574
QY 551 euLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuI 571
Db 2575 TTTTGATCTCTCCTTCCTGATCAATGAATATGAATGATGATGATGATGATGATGATGATGAT 2634
QY 571 leAsnGlyGlyGlyLeuLeuGluLeuThrValPheProAlaLysTySerMetGluMetS 591
Db 2635 TCAATGCTGTGGAGTGGAGAGACACAGATTTTTCATCAAAAGTATGCCATGGAAATGT 2694
QY 591 erAlaValValTyLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleL 611
Db 2695 CATCTGTTGTTTACAAGACTGGGTCTTACTAGCAAGACACTTCTGCTGATCTCATCA 2754
QY 611 ys----- 611
Db 2755 A-GAGTATATAAATACTGTTAGTGAATGTTTCTTCTGCTGCTGGAATGAATCTAGTG 2813
QY 612 -----ArgGlyVala 615
Db 2814 AAAATTGATTTTTCATCTAATGATATGCTGCAACTTGGGCACCTCTTTTCAGAGGAATGG 2873
QY 615 laValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyProTyra 635
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QY 635 laValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyTyCysAsnT 655
Db 2934 CTGTTGATGGACTTGAATCTGCTGAGCTATTGACATGCTGGTGAAGAGTATTGCTCAT 2993
QY 655 yrTyTyTySerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysG 675
Db 2994 TCTACTACAAGACAGATGAGTGGTCCAGAAAGACTCTGAGCTTCAGTCTGCTGGTGAAGG 3053
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QY 675 luLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnT 695
Db 3054 AAGTCAGGAGAGAGGTCATGGCGACAGAGAGGAGCCCTGGTGGCTAAATGCATA 3113
QY 695 hrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisA 715
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QY 715 laAlaValAsnPheGlyGlnTyProTyAlaGlyTyLeuProAsnArgProThrLeuS 735
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QY 735 erArgAsnPheMetProGluProGlySerProGluTyTyGluGluLeuLysThrAsnProA 755
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QY 755 spLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuI 775
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RESULT 4
US-09-938-842A-1504
; Sequence 1504, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1504
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1504

Alignment Scores:
Pred. No.: 0 Length: 2580
Score: 3202.50 Matches: 2580
Percent Similarity: 82.79% Conservative: 122
Best Local Similarity: 68.71% Mismatches: 138
Query Match: 70.63% Indels: 11
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QY 18 LysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsn 37
DB 58 AGGTGAAGGAAAGCGTGTCTGATGAAGAAGACGCTCTCGATTTCAACGATTTCAAT 117
QY 38 AlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIle 57
DB 118 GCTTCGTTCTCGATCGTCTCATGAATTTCTCGAAACAAATCACTCTTCGCTTGT 177
QY 58 SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaIleTyr 77
DB 178 AGCTCTGATGTTACTGATTCAGAAACCGGTTCTAAAGGCAAACTAGGGAAGGCTGCTCAC 237
QY 78 LeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgVal 97
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QY 98 ThrPheAspTrpAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeu 117
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DB 415 GTCCATTACATCTGAATCTCTGGATTTACCTCTGCTAAACACTACACACAGCCAGGTC 474
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DB 535 GAAAGAGAGCTAGTGAGTGTGAGAGAACCGCGGAGGAGAGCTTAAAGGAATGGGACAGA 594
QY 198 ValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSer 217
DB 595 GTATATGACTATGCTTACTACATGATTTAGCGGTCCTCCACCAAGAAC-----CCA 645
QY 218 ArgProValLeuGlySerSerGluTyrProTyrProArgArgGlyValThrGlyArg 237
DB 646 CGGCTGTACTTGGAGGACACAGGAGTATCTTACCCCAAGAGAGGAGAACCGGGCGG 705
QY 238 LysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAsp 257
DB 706 AAACCAACTAAAGAGATCTCTCAACCGAGACAGCGTACCAGTACATCATCGAGCCTAGAC 765
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DB 766 ATATATGTTCCAGAGATGAGAGATTTGGACATTTGAAGATGCTGATTTCTTCCTTCT 825
QY 278 AlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThr 297
DB 826 GCTCTAAAGCGATTTGCTCAGTTTCATCCACCTGACCTTGAGGCTGTATTTCAGCATACT 885
QY 298 HisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeu 317
DB 886 CCTAAGAGGTTGATTTCTTTGAAGATGTTCTTAAGATCTATGAAGAAGGAATCGATCTA 945
QY 318 ProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLysGlu 337
DB 946 CCAACCAAGCTTTGATGATAGTTCGTTAAGATATATACCGCTTGAGATGTTAAAGGAG 1005
QY 338 LeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGlu 357

DB 1006 ATATTTCAGAACAGATGGCCAGAAATTTCTTAAGTTTCCAGTGCCTCATCAAGAG 1065
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DB 1066 GACAAACTGTCATGAGAACAGATGAGAAATTTGCTAGAGAAATTTGCTGCTGAGCTAAAC 1125
QY 378 ProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIle 397
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QY 518 HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaIleGluProPheValIleAla 537
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DB 1600 ACAAACAGACAGCTGAGTGTCTTCACCCGCGTCTTTAAGCTCTTTGAACCTCAGCTCCG 1659
QY 558 GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeu 577
DB 1660 GATACGATGAATATCATGCACTTCTAGGCAAAATCTTGATCAATGGTGGTATATTT 1719
QY 578 GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp 597
DB 1720 GAAATCACTGTGTTCTTCTTAATATCCCATGAGATGTCATCTTTCATTTACAAAAAC 1779
QY 598 ---TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616
DB 1780 CACTGGACCTTCCCTGACCAAGCATTTACAGCAGAACTTAAAGAGAGAGGATGCGCGT 1839
QY 617 GluAspSerSerSerProLeuGlyIleLeuLeuLeuIleGlnAspTyrProTyrAlaVal 636
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QY 637 AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyr 656
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QY 657 TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu 676
DB 1960 TACAAGATAGAGGAGATATCCAAACCCACACAGAGCTCCAAAGCCTGGTGGAAAGAGGTG 2019
QY 677 ArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrVal 696
DB 2020 CGCAGGAGGTCTAGGAGACAAAGTCAGAACCATGCTGGCTTAAATGCAAAACCGT 2079
QY 697 GlnGluLeuIleAspSerCysThrIleThrIleAlaSerAlaLeuHisAla 716

Qy	378	ProVallleSerArgLeuGlnGluPheProProLysSerLysLeuAppProLysle	397
Db	1126	CCTGTTGTTATTCAACTCTTTAAGAGAGTTCTCTCCAAAGAGTAAGCTTGACAGTGAATCA	1185
Qy	398	TyrGlyAsnGlnAanSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeu	417
Db	1186	TACGGTAACCGAACAGATACATCACTAATAGCCACATAGACACAAATTTGGATGGACT	1245
Qy	418	ThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeu	437
Db	1246	ACTGTTGAAGAGGCTCTGGAGAGGAGGTTGTTTATATTAGACACCATGACACACTG	1305
Qy	438	MetProTyrIleuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThr	457
Db	1306	ATGCCATACTTGGGACCGGTAAACACACACACG---ACCAAGACTTATGCAACGAGACA	1362
Qy	458	LeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuPro	477
Db	1363	CTTCTGTTCTTGAAGATGATGGACCTTGAAGCGTTGGTGATAGAGCTGAGCTTGCCT	1422
Qy	478	HisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGly	497
Db	1423	CATCCTAATGGAGACAAATTTGGAGCAGTGAGTGAAGCTATATACGCTGCT---GAAGGT	1479
Qy	498	ValGluGlySerIleTrrGlnLeuAlaIysAlaTyrAlaValaValaAsnAspSerGlyVal	517
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Qy	518	HisGlnLeuIleSerHisTrrLeuAsnThrHisAlaAlaIleGluProPheValIleAla	537
Db	1540	CATCAGCTTATTAGCCACTGGATGCCAAACACACGCATCGATTGACCGTTTGATGTGCC	1599
Qy	538	ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg	557
Db	1600	ACAAACAGACAGCTGAGTGTCTTTCACCCGCTCTTAAAGCTCCTTGAACCTCACTCCGT	1659
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Qy	578	GluLeuThrValPheProAlaLysTrrSerMetGluMetSerAlaValValTyrLysAsp	597
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Qy	617	GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal	636
Db	1840	GAGATCCAGAACACACACCGAATTACGTCGTAGGATAAAGACTATCTTACGAGTG	1899
Qy	637	AspGlyLeuLysIleTrrPsrAlaIleLysSerTrrPValThrGluTyrCysAsnTyrTrr	656
Db	1900	GATGGCTTCGAGTTGTTGATGCTATTGAATCATGGTCCGAGACTACATTTTCTTCTTC	1959
Qy	657	TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrrTrrLysGluLeu	676
Db	1960	TACAAGATAGAGGAGGATATCCAAACCGACACAGAGCTCCAAGCTTGGTGGAGAGGTG	2019
Qy	677	ArgGluGluGlyHisGlyAspLysLysAspGluPrrProTrrPrrProLysMetGlnThrVal	696
Db	2020	CGCAGAGAGCTCATGAGACAAAGATCAGAACCATGTGGTGGCTTAAATGCAAAACCCGT	2079
Qy	697	GlnGluLeuIleAspSerCysThrIleThrIleTrrPileTrrAlaSerAlaLeuHisAlaAla	716
Db	2080	GAAGAACTTGTGAGCTTCACCATCATTTTGGTGGCTTCTGCTTCTCATGAGCT	2139
Qy	717	ValAsnPheGlyGlnTrrProTrrYAlaGlyTrrLeuProAsnArgProThrLeuSerArg	736
Db	2140	GTTAACCTCGGACAGTATCCAGTTGCTGGGTACTCCCAACAGACCGCATTAAGCCGT	2199

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Qy	757	ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuLeuGlu	776
Db	2260	GTGTTTTTGAGACCATCACAGCTCAGCTTCAGACACTTCTAGGATATATCTTGATTTGAG	2319
Qy	777	IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyr	796
Db	2320	ATTCTCTCTACTCTATTCTAGCGAGGCTCTATTTCGGACAGAGAGATTTCTAAAGAAATGG	2379
Qy	797	ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle	816
Db	2380	CGCGCTCAGAGAAGAAGCGTTTGGAGGCCCTTCGAAAGTTTGGAGAGAAGTAAAGGAGATT	2439
Qy	817	GluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProVal	836
Db	2440	GAGAAGAACATTTGATGAGAGAACGACGACGAGACTCTCAAGAACAGGACTGGTTTGGTT	2499
Qy	837	LysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle	856
Db	2500	AAGATGCCATACACTTTATTGTTTCCGAGCAGTGAAGCGGAGTCCACCGCAGGGAATT	2559
Qy	857	ProAsnSerValSerIle	862
Db	2560	CCAAATAGCGTCTCTATC	2577
RESULT 6			
US-09-978-522-2			
; Sequence 2, Application US/09978522			
; Publication No. US20030033627A1			
; GENERAL INFORMATION:			
; APPLICANT: Descenzo, Richard			
; APPLICANT: Irelan, Nancy			
; TITLE OF INVENTION: Lipoxxygenase Genes From Vitis Vinifera			
; FILE REFERENCE: 29520/37890			
; CURRENT APPLICATION NUMBER: US/09/978,522			
; CURRENT FILING DATE: 2001-10-16			
; PRIOR APPLICATION NUMBER: 60/241,220			
; PRIOR FILING DATE: 2000-10-16			
; NUMBER OF SEQ ID NOS: 45			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 2			
; LENGTH: 4687			
; TYPE: DNA			
; ORGANISM: Vitis LOX 1			
US-09-978-522-2			
Alignment Scores:			
Pred. No.: 0 Length: 4687			
Score: 3138.00 Matches: 652			
Percent Similarity: 56.19% Conservative: 110			
Best Local Similarity: 48.08% Mismatches: 96			
Query Match: 69.21% Indels: 502			
DB: 10 Gaps: 10			
US-10-731-642A-1 (1-862) x US-09-978-522-2 (1-4687)			
Qy	3	LeuGluLysIleValAspAlaIleThrGlyLysAspAspGlyLysLysValLysGlyThr	22
Db	13	CTTCTTTCAATTGTTAGTGCCACTCCTGGGAAAATGATAAAGAAGAAGATCGAGGGAAC	72
Qy	23	ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnIleSerValLeuAsp	42
Db	73	ATTGTGTGTGATGAAGAAGAAATGTTGGATTTTAAATGACTTCAATCGCCGGTCCGGAC	132
Qy	43	GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerValAsnAla	62
Db	133	CGGGTTTCATGAGCTTTTGGACAGGAGAGTCTCTCGAGCTGCTGCTGCTGCTGCTGCTG	192
Qy	63	AspPro-----	64

Db 193 GATCCTGGTGAGTGTGTTTTTTTTTTTTTTTTTTTTTCTTCATGTTTTTTGATGATGGGTGTTG 252
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Db 253 AAGTTGGAGGAGGAGGTGATACCGTTTTGTGAGGGTGAGATGGGTTCGAAATTTGA 312
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Db 313 TGATAGCAATTTGGAAAAAGATGTGATTTTTTGGAGAGGCCAAGAGGGGTGTTATTCTCA 372
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Db 373 GAGATGAGTCAAAATGACTTCTTGACATCTTCCATTCAACTGGGCACATTTTCTTAAGTCT 432
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Db 433 TTTGTTTTTGTGTTTTGTTTTTAATGCTTTTTTGTCTTCTACTTCTTCTCTGTTATAT 492
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Db 493 TTTCTTTTCATCAACCATAFACATGCCACCTAACTCAATATGAAATTCCTCATGACGTG 552
Qy 64 ----- 64
Db 553 CCCTTTTTTTAAAGCCACTAGATCTTGGGTGATTTTTTTAGTCTTAGATCTTTGGGTAGAT 612
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Db 913 TGTGCTTTTGTAGCAATGGGTTACAGGGGAAACTTGGGAAACCCAGCATACTTTGGAAGA 972
Qy 80 nTriLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAs 100
Db 973 CTGGATTACCAATTTACTTCTTTAAACCGCTGGCGAGTCTGCATTTCAAGGTCAAGTTCGA 1032
Qy 100 pTriAspAspGluGluPheGlyValProGlyAlaPheIleLeuLysAsnLeuHisPheSe 120
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Qy 120 rGluPhePheLeuTyrSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPh 140
Db 1090 TGAGTTTTTACCTCAGGACTCTCACTCTTGAAGATGTTCTCGACGTGCGAGAATTCACCT 1149
Qy 140 eValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAl 160
Db 1150 TGTTTGTAAATCTCTGGGTCTACCCCTGCTAAGCACATACAAAACCTGACCGTGTCTTCTCAC 1209
Qy 160 aasn----- 161
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Qy 162 -----GlnAl 163
Db 1270 TGAGCTTAGGCAAGGAGAATTGTCTGCTAAAGGAATGTGTTTTATTTTATCTGCTGCAGAC 1329

Qy 163 aTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAenGluLeuValTh 183
Db 1330 ATATCTTTCCAAAGTGAAACACCCAGGGCCACTCGCGAAGTACAGAAAGGGGAACCTGGTGA 1389
Qy 183 rLeuArgGlyAspGlyThrGlyLysLeuGluGluTirAspArgValTyrAspTyrAlaTy 203
Db 1390 TCTGAGGGAGATGGAACCGGAGAGCTTAAGGAATGGATCGAGTGTATGACTATGCTTA 1449
Qy 203 rTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGl 223
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Qy 223 ySerSerGluTyrProTyrProArgGlyArgThrGlyArgLysProThrLys---- 241
Db 1510 ATCTGCAGAGATATCCTTATCCAGAGGGGAAGAACTGGTAGACCACCATCTGAAAGG 1569
Qy 241 ----- 241
Db 1570 TAGATATTTGATACACAAATTCATATTTGTTTCTCATGCTTTTATCATAAAAGGATGAATA 1629
Qy 242 -----ThrAspProAsnSerGluSerArgIleProLe 252
Db 1630 TGATTTGATTTCTGCTCTTCTTTTAAATTAACAGATCCCAAACTGAGAGCAGATTGCCACT 1689
Qy 252 uLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSe 272
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Qy 272 rAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuProGluPheLysAl 292
Db 1750 AGACTTCTGCTGTTATGCCCTGAAATCCATAGTTCAATTCCTCTCCCTGAGTTTGAGGC 1809
Qy 292 aLeuPheAspSerThrHisGlnGluPheAspSerPheGluAspValLeuLysLeuTyrGl 312
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Qy 312 uGlyGlyIleLysLeuProGlnGlyProLeuLysAlaIleThrAspSerIleProLe 332
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Qy 332 uGluIleLeuLysGluLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrPr 352
Db 1930 TGAGATGCTCAAGAACTTGTGTCGATCCGATGGGGAACATCTCTTCAAGTTCCCAATGCC 1989
Qy 352 oGlnValIle-Gln----- 356
Db 1990 CCAAGTCATCAAGGTACTGCATACATCTTGTAAATCTTTGAAGCCAGATTTAT 2049
Qy 357 -----GluAspLysThra 361
Db 2050 ATATTTATTTTTCATAAAATTTGATGACGTTTTTATCATGCTGGAGCAGAGATAGTCTG 2109
Qy 361 laTriArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleI 381
Db 2110 CATGAGGACTGACGAAGAATTTGCTAGAGAAATGCTGGCTGGACTCAACCCAGTTGTCA 2169
Qy 381 leSerArg----- 383
Db 2170 TCCG-TCCTACTCCAAGTAAACTACAGCTTCCTTTCAAATAATTTTAAATGCCCTGTTGT 2228
Qy 383 ----- 383
Db 2229 TTTCTGAGAAATGGAACCTGGAAAGGCTTCCAGACTTTGTTTCTTCTTCCCTCCATCTAC 2288
Qy 384 -----LeuGlnGluPheProp 389
Db 2289 TGTCTAGCTCTTTTCTGATAATTTATTTGCTCTTCTTCTTCTTGTGTTGAAGGAGTTCTCTC 2348
Qy 389 roLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluG 409
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QY 409 InilecluaSpLysLeuAspGlyLeuThrIleAspGluAla----- 422
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QY 422 ----- 422
Db 2468 CTTTCAAACTAAATTTTCAATGTGACATGTTAATTTTTCATTTGGACAACAAGCCAT 2527
QY 423 -----IleLysThrAsnArgLeuPheIleLeuA 432
Db 2528 AGTAACGTGAAAATGGTGTCTTTTACTAGGCAATGGAGAGAGGCTTATTCATATTAG 2587
QY 432 snHisHiaSpIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysT 452
Db 2588 ATCCACATGATGTTTTCATGCTACCTGAGGAGGATAAACA---ACTTCCACGAAA 2644
QY 452 hrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaI 472
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QY 512 alaAspSerGlyValHisGlnLeuLeuIleSerHisTrrpLeu----- 525
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QY 525 ----- 525
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QY 604 laLeuProThrAspLeuIleLys----- 611
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QY 611 ----- 611
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QY 612 -----ArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeuL 628
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QY 628 euileGlnAspTrrpProTyrAlaValAspGlyLeuLysIleTrrpSerAlaIleLysSert 648
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QY 648 rpValThrGluTrrpCysAsnTrrpTrrpLysSerAspAlaValGlnLysAspThrG 668
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QY 708 rpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTrrpProTyrAlaGlyTrrL 728
Db 3603 GGGTGGCTTCTGCTCTCCATGCTGAGTGAATTTCCGGCAGTACCTTATGAGGCTACC 3662
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US-10-425-114-11204
; Sequence 11204, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11204
; LENGTH: 2828
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701040644_FLI
US-10-425-114-11204
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Score: 3104.50 Matches: 578
Percent Similarity: 82.18% Conservative: 123
Best Local Similarity: 67.76% Mismatches: 139
Query Match: 68.47% Indels: 13
DB: 17 Gaps: 8
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US-10-731-642A-1 (1-862) x US-10-425-114-11204 (1-2828)

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Db 52 AAGAGGGTTAAAGGAGAGTGGTTTGAAGAGAGGGTGTGGATCTCCACAGATC 111
Qy 37 AsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLysLeuLeu 56
Db 112 AAAGCCACGTTCTCGATCGAGTTACACAGTTATTAGGCAAGGGTGTCTCTTCAGCTT 171
Qy 57 IleSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAla 76
Db 172 ATTAGTGCTACTACTCTCTGATCCAGCAAGGGGTTA-----TTGAGAGGGGAAGGTGCA 225
Qy 77 TyrLeuGluAsnTyrLeuThrAsnSerThrProIle-----AlaAlaGlyGlySerAlaPhe 95
Db 226 AACTTGGAGAGGTGGGTTTTCAGCATTTACCTCTTTGACATCAACACAGACACAGAGTTC 285
Qy 96 ArgValThrPheAspTyrAspGluPheGlyValProGlyAlaPheIleLys 115
Db 286 TCAGTTACATTTAGTGG--GATGAGAGCATGGGTGTCTCTGGGGCATTCATAATCGA 342
Qy 116 AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis 135
Db 343 AACATCACCATAGCCAGTCTTACCTCAAGACACTGACCATTTGAAGACATTCACAGGCAT 402
Qy 136 --GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSer 154
Db 403 GATGTCCTGTTAATTTTGTCTGCAATTTCTTGGGTCTACCTGCTCATCTTACGCCCAT 462
Qy 155 AspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArg 174
Db 463 GATCGTGTCTTTTGGCAACAAGGCTTATCTTCCATGTCATACACCTGAGCCACTGGCG 522
Qy 175 LysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGlu 194
Db 523 AAGTTTCAGGAAACAGAACTCTCTCGCGGAAAGGTTTCGGGAAGCTTAATGAG 582
Qy 195 TrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGln 214
Db 583 TGGGACAGAGTCTATGACTATGCTACTACATGATTTGGGACTTCCAGATGATGGTCT 642
Qy 215 AspLeuSerArgProValLeuGlyLysSerGluTyrProTyrProArgGlyArg 234
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Qy 255 SerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPhe 274
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Qy 295 AspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGly 314
Db 877 GACAAAACATTAATGATGAGTTTGACACCTTTCAAGATGTACTTGAATTTATGAGGGAAGT 936
Qy 315 IleLysLeuProGlnGlyProLeuLysAlaIleThrAspSerIleProLeuGluIle 334
Db 937 ATTAAAGTGCACAGTGGACCTTTACAGAGTAAACTGAGAAAACCTGTTCCCTATGAGCTA 996
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Db 997 TTGCGAGAACTTATTAGGAATGATGTTGAGAGATTCCTCAAATTCCTCGCTGCTGATGTG 1056
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Db 1057 ATCAAAGTGAGTAAGACAGCATGGAGGACAGATGAGGAATTTGCAAGGGAATGCTTCA 1116

Qy 375 GlyValAsnProValIleIleSerArgLeuGlnGluPheProLysSerLysLeuAsp 394
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Qy 395 ProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeu 414
Db 1177 CCCAGCGTATATGAGACCAAACTAGCTCCATCAGACGACGACCATAGAAAATAGTTTG 1236
Qy 415 AspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHis 434
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Qy 515 SerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaIleGluProPhe 534
Db 1534 TCAGGATATCATCAATTTGGTTAGCTTACACTGCTGTTATACACTCACGCAAGTAATTTGAACCGTTC 1593
Qy 535 ValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisPro 554
Db 1594 ATTATGCCCAACACAGCGCAGTTGAGTATTTCTTCCCAATACACAGCTCTTGAAGCCA 1653
Qy 555 HisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGly 574
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Db 1714 GGGGTACTAGAGATTACAGTTTCCCTGGTAAATTCGCTTGGAAATGCTCGCTGTTATA 1773
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Db 1774 TACAAAAGTTGGGTATTACACGAGCAGCACTACTGCTGATCTTCTTAAAGGGGGAATG 1833
Qy 615 AlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyr 634
Db 1834 GCAATTCCTGATTCAGTTCTCGTCATGGACTAAGGCTTGTGATAGAGGATATATCCGTTT 1893
Qy 635 AlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsn 654
Db 1894 GCCGTGACGCGCATAGAAATCTGGGATGCAATAGAAACCTGGGTGACTGAAATCTGTAAAC 1953
Qy 655 TyrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLys 674
Db 1954 TTCATTATACATCCCAATGACATGCTCGAGGAACAGACTGAACTTCAGAGTTGGTGGAAA 2013
Qy 675 GluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTyrTrpTrpProLysMetGln 694
Db 2014 GAAGTACGCAACGAGGTCACGGTGACTTAAAGATAGGAATTTGGTGGCAGACATGAAG 2073
Qy 695 ThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHis 714
Db 2074 ACCAAGAGGAACCAITTCATTATGACCATTCATATGCTTTCGCTTCTGCTATTCAT 2133
Qy 715 AlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeu 734
Db 2134 GCAGCTGTGAATTTTGGACAGTACCCCTTTTGGATACCTCCCTTAACCGGTCACCGGTG 2193
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Db 2254 GAATGGGCAATTCCTCAAAACAATCACTGCGCAGTTTCCAAACACCTTGTGTGTGTCTACTG 2313
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Db 2494 CCGGTGAAGATCCCTTACACACTTCTTATCCCAACACCTCAGATTATTTCTAGGAGGGT 2553
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RESULT 8
US-10-424-599-70317
; Sequence 70317, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 70317
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_34507C.1
US-10-424-599-70317

Alignment Scores:
Pred. No.: 0 Length: 2867
Score: 3087.50 Matches: 577
Percent Similarity: 82.20% Conservative: 125
Best Local Similarity: 67.56% Mismatches: 138
Query Match: 68.10% Indels: 14
DB: 17 Gaps: 8

US-10-731-642A-1 (1-862) x US-10-424-599-70317 (1-2867)
Qy 17 LysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIle 36
Db 85 AAGAGGGTTAAGGAGAGTGGTTTGTATGAAGAGGGTGTGTGACCTTCACAGACATC 144
Qy 37 AsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeu 56
Db 145 AAAGCAACGTTCTCGATCGAGTTCACAGTATTATTAGGCAAGGGGTCTCTCTCAGCTT 204
Qy 57 IleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAla 76
Db 205 ATTAGTGCTACTACTCTCTGATCCAGCAAGGGGTTA-----TTGAGAGGGGAAGGTGCA 258
Qy 77 TyrLeuGluAsnTrpLeuThrAsnSerThrProIle-----AlaAlaGlyGluSerAlaPhe 95
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Db 259 AACTTGGAGAGGTGGTTTCGACGATTACCTCTTTGACATCAACAACACACAGAGTTTC 318
Qy 96 ArgValThrPheAspTrpAspAspGlnGluPheGlyValProGlyAlaPheIleLys 115
Db 319 TCAGTTAGCTTTGAGTGG---GATGAGAGCATGGGTGTCTCTGGGGCATTTCAATAACCGA 375
Qy 116 AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis 135
Db 376 AACAACTACCATAGCCAGTTCTACCTCAAGACACTGACCATTTGAAGACAAATTCAGGGCAT 435
Qy 136 ---GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSer 154
Db 436 GATGTCCTCTGTTAAATTTGTCTGCAATTTCTTGGGTCTACCTCTGCTCATCGTTACGCCAT 495
Qy 155 AspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArg 174
Db 496 GATCGTGTCTCTTTTGGCCAAAGGCTTATCTTCCATGTCTATACACCTTGAGCCACTGGCG 555
Qy 175 LysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGlu 194
Db 556 AAGTTCAGGGAACAAGAACTAAACTCTCTCGGGGAAAGGTTTCGGGAAGCTTAAATGAG 615
Qy 195 TrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGln 214
Db 616 TGGGACAGAGCTATGACTATGACTATCAATGATTTGGGACTTCCAGATGATGTCCT 675
Qy 215 AspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArg 234
Db 676 GACTATGACGCGCTGTCTTGGAGGA---TCACAAATTTCCATATCCACGTAGAGGAAGA 732
Qy 235 ThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMet 254
Db 733 ACTAGTCTCCACATVTGCAAAACAGATCCTAAACTGAGTCAAGATTGATCTTCTA--- 789
Qy 255 SerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPhe 274
Db 790 AATCTAAACGTTTATGTCCGAGGAGTGAACAGTGTGGCCATGTCAAGTTTTCAGATT 849
Qy 275 LeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPhe 294
Db 850 CTGGCATACTCACTGAAATCTGTCTCAGGTTTGTCTTCCAGAGATTAAATCTTTGTGT 909
Qy 295 AspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGly 314
Db 910 GACAAACTATTATGAGTTTGACACCTTTGAAGATGACTTGATATTATGAGGGAAGT 969
Qy 315 IleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIle 334
Db 970 ATTAAGCTTCCAAGTGGACCTTTAGCAGATAAAGTGAAGAACTTGTTCCTATGAGCTG 1029
Qy 335 LeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnVal 354
Db 1030 CTGAGAGAACTTATTAGGAATGATGTGAGAGATTCTCTCAAAATTCCTCGGTGCTGATGTG 1089
Qy 355 IleGlnGluAspLysThrAlaTrpArgThrAspGluPheGlyArgGluMetLeuAla 374
Db 1090 ATCAAGTGAGTAAAGACTGCATGGAGGACAGATGAGGAATTTGCAAGGGAATGCTTGA 1149
Qy 375 GlyValAsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAsp 394
Db 1150 GGGGTTAACCTCTTATTATTCGCGCTCTTCAGGAATTTCCCGCGCCAGCAAGCTAGAC 1209
Qy 395 ProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeu 414
Db 1210 TCCAGAGTCTATGAGACAAACTAGTTTCCATCAGACCAAGCCACATAGAAAATAGTTG 1269
Qy 415 AspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHis 434
Db 1270 GATGGGCTTCAATAGATGAGGCAATTCAAATATGAGGCTATTATATTATAGATCATCAC 1329
Qy 435 AspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLys--ThrTyrAl 454
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1330 GACTCATTGATGCCATACATTAGTCGAATAAAC---TCTCAACACACAAAGAACTTATGC 1386
454 aSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLe 474
1387 CTCTAGAACGCTCCTGTTTCTACAGATGACGGGTACACTCGAGCCACTGGCTATAGAGTT 1446
474 uSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValThrProAl 494
1447 AAGCTTACCCATCCACCAAGGGGAAACAATGAGAGCTGTGAGCAAGTTTTCATCTCCAGC 1506
494 aAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaValAsnAs 514
1507 ACAAGAAGGAGTATCGGCTTGGCTGGCAGCTGCTTAAGGCTTATGAGCGGTCAATGA 1566
514 pSerGlyValHisGlnLeuLeuSerHisTrpLeuAsnThrHisAlaIleGluProPh 534
1567 TTCAGGATATCATCAATGGTTAGCCACTGGTTATACACTCAGCAGTAATTTGAACCGTT 1626
534 eValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyTrpLysLeuLeuHisPr 554
1627 CATATAGCCACAAACAGCAGCTGAGTATCTTCACCCAAATACAAAGCTCTTGAAGCC 1686
554 oHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyG 574
1687 ACACCTTCAGGACACAATGCATATAAATGCCTTAGCCCGCACACGCTCATCAATGCTGG 1746
574 yGlyLeuLeuGluLeuThrValPheProAlaLysTyTrpSerMetGluMetSerAlaValVa 594
1747 AGGGGTACTAGAGATTACAGTTTCCCTCGTAAATTCGCTTGGAAATGCTGCTCGTTAT 1806
594 lTyTrpLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyVa 614
1807 ATACAAAAGTTGGGTATTACCGACAGCAGCTACTCTGCTGATCTTCTTAAGAGGGGAAT 1866
614 lAlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyTrpPro 634
1867 GGCATATCTGATTCAGTTCTCGTCATGAGTAAAGCTTGTGATAGAGGATTATCCGTT 1926
634 rAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyTrpCysAs 654
1927 TGCCGTGACGCGCATAGAAATCTGGATGCAATAGAAACCTGGGTGACTGAATCTGTAA 1986
654 nTyTrpTyTrpLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLys 674
1987 CTTCATTATACATCCATCATGATCGTTCGAGGAACAGTGAATCTAGAGTTGCTGGA 2046
674 sGluLeuArgGluGluGlyHisGlyAspLysAspGluProTrpTrpProLysMetG 694
2047 AGAAGTACGCAACGAGGGTTCACGGTGACTTAAAGATAGGAATTCGTCGCCAGACATGAA 2106
694 nThrValGlnGluLeuLeuAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHi 714
2107 GACCAAGAGGAACTCAATTCATTCATGACCAATATCATATGCTTGTCTGCAATTCGA 2166
714 sAlaAlaValAsnPheGlyGlnTyTrpProTyTrpAlaGlyTyTrpLeuProAsnArgProThrLe 734
2167 TGCACTGTGAATTTTGGACAGTACCTTTTCTGATACCTTCCCTACCTACCTCCACCGT 2226
734 uSerArgAsnPheMetProGluProGlySerProGluTyTrpGluGluLeuLysThrAsnPr 754
2227 GAGTCGTAGTTTCATGCCGGAAGGTAACCCAGAGTATGAGGAGCTTAAGTCAGACCC 2286
754 oAspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerIle 774
2287 TGAATTTGGCATTTCTCAAAACAATCACTGCCAGTTTCCAAACACATTTGTTGGTGTCTACT 2346
774 uIleGluIleLeuSerArgHisSerAspThrLeuTyTrpLeuGlyGlnArgGluSerPr 794
2347 GATAGAGTTCTGTCCAGCATCTCACTGAAGAGGTTTACCTTGGGCAATGTGAGAACCC 2406
794 oGluTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLeuLeuSe 814
2407 TGAATGGACTCTAGATGCTGAGCCATTGGCAGCAATTTGAGAGGTTTTCAGACAGAGCTGTT 2466

814 rAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGl 834
2467 GGAGATTGAGAACAAATATCATGGAAAGAACACAGAACAGAGATTCAAAAACAGAAATGG 2526
834 yProValLysValProTyTrpThrLeuLeuPheProThrSer-----GluGl 849
2527 GCCGGTGAAGATGCTTACACACTTCTCTATCCCAACACCTCAGATTATTCTAGGAGGG 2586
849 yGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
2587 TGGACTAACTGGCAAGGAATCCCAACAGTATATCCATC 2626

RESULT 9

US-10-059-909-11
; Sequence 11, Application US/10059909
; Publication No. US20030074693A1
; GENERAL INFORMATION:
; APPLICANT: Caboon, Edgar B.
; APPLICANT: Kinney, Anthony
; APPLICANT: Klein, Theodore
; APPLICANT: Lee, Jian Ming
; APPLICANT: Pearlstein, Richard
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Shen, Jennie
; APPLICANT: Thorpe, Cathy
; APPLICANT: Tingey, Scott
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Lipoxigenases
; FILE REFERENCE: BBI333 US CIP
; CURRENT APPLICATION NUMBER: US/10/059,909
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/501,422
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/119,597
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 2929
; TYPE: DNA
; ORGANISM: Momordica charantia
US-10-059-909-11

Alignment Scores:
Pred. No.: 1.94e-312 Length: 2929
Score: 3022.50 Matches: 554
Percent Similarity: 80.99% Conservative: 132
Best Local Similarity: 65.41% Mismatches: 156
Query Match: 66.66% Indels: 5
DB: 14 Gaps: 4

US-10-731-642A-1 (1-862) x US-10-059-909-11 (1-2929)

16 GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp 35
126 GGGAGAGAGATCAAGGACGGTGGTCTTATGAGAGCAATGTTTGACCTTCACCGAA 185
36 lIleAsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGlu 55
186 TTTCAATCCTCACTTCTTACGGGCTCACTCAGCTCTTGGCGCGGAAATTTTCATTGCAA 245
56 LeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAla 75
246 CTTATCATGTGTACTCAGCT-----TCCAAACGACTCGCGAGGAAAGTTGGAAAGGGG 299
76 AlaTyTrpLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyLysSerAlaPhe 95
300 CGGTTCCTGGAGAGGTGGCTGACTTCAGTCCGCCACTGTTCCGCTGGAGAGTCTGTGTT 359
96 ArgValThrPheAspTrpAspAspGluPheGlyValProGlyAlaPheIleLys 115
360 CAAGTGAACCTTTGATTGG---GAAGAGAACTTTGGATTTCAGGAGCTTTCTTCAAAA 416

116 AsnLeuHisPheSerGluPhePheLeuLeuLeuSerLeuThrLeuGluAspValProAsnHis 135
117 |||||
417 AATGGCACACACAGTGGTCTTCCTCAAGTCTGTAACTCTGGAGATGTTCTGGCTTT 476
136 GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAsp 155
137 |||||
477 CGAAGGGTCCATTTTGACTGCAACTCATGGTTTACCCTTCTCGAAGATACAGAAGAT 536
156 ArgIlePhePheAlaAsnGlnLatyrLeuProSerGluThrProAspThrLeuArgLys 175
157 |||||
537 CGCATTTCTTTGCCAACATACATCCCTTCCAAATGATACACCGGATTCACCTCGTAAG 596
176 TyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTrp 195
177 |||||
597 TATAGAGAGAGAGTGTGTGAACCTCAGAGGAGATGGACAGAGAGCGGTAAAGATGG 656
196 AspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAsp 215
197 |||||
657 GATAGAATTTATGACTATGATGTTTACAACGACCTCTGTGATCCAAATGGTGCCTAAC 716
216 LeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThr 235
217 |||||
717 CTTGTTCGTCCTATTCTCGAGGAGTGTATCAGTACCCTTACCCTCGTAGAGGGAGACA 776
236 GlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSer 255
237 |||||
777 GGAAGACACCGCTGAGAAAGATCAAGTAGCAGAGCAGATGTTCGGATGTGATGAGC 836
256 LeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeu 275
257 |||||
837 TTAACATTTTACGTACCGAGAGACGAAATTTTCGGACACTTGAAGATGCGGATTTCCCT 896
276 ThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAsp 295
297 |||||
897 GGAATACGTTGAAGTACTTCTACATCTATCCACAGGACTTGAATCTATATTGAT 956
296 SerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIle 315
297 |||||
957 TCACCCAGGAGAAATTCACAAATCAAGAAAGTAGACGATCTCTTTGAAGCAGGGTTT 1016
316 LysLeuProGlnGlyProLeuLysAlaIleThrAspSerIleProLeuGluIleLeu 335
337 |||||
1017 CCCATTCCATTGAAT--ATTTTAAAGAACCTCACAGAGGACCTCGCCCCCCTCTTT 1073
336 LysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIle 355
357 |||||
1074 AAAGCATTTCTGAGGAGTGTGTGAAGATTCCTCAAAATATCCAACTCCCAAGTTATC 1133
356 GlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGly 375
377 |||||
1134 AAAGATAACAGTTAGGTGGAGGACAGATGAAGAAATTTGCCAGAGAAATGATAGCGGA 1193
376 ValAsnProValIleLysSerArgLeuGlnGluPheProProLysSerLysLeuAspPro 395
397 |||||
1194 GTCAATTCCTTTCATTCGTCGTCCTTGAAGTTTTCACCACTTGAAGTTGAGCCCT 1253
396 LysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAsp 415
417 |||||
1254 CATGTTTATGGGAATCAAAACAGTACAAATGACGGAGAGAACAAATAAAGCATGTTAGAT 1313
416 GlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAsp 435
437 |||||
1314 GGACTACCGTTTGTAGAGCAATCAAGAAATATAGCTCTACATATTGGATCACCATGAT 1373
436 IleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSer 455
457 |||||
1374 GCATTGATGCCATATCTTAGGAGATAAAT--TCAACATCTACAAAACATATGCCACA 1430
456 ArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSer 475
477 |||||
1431 AGAACACTTCTCTTTTGAAGATGACAGTACTTTGAAGCCATTCGCTATTGAGTTGAGC 1490

476 LeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAsp 495
497 |||||
1491 TTGCCACACCCGACAGAGATGAACATGGTGCATAGCAAACTATACTTTCCAGCTGAA 1550
496 GlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValaAsnAspSer 515
517 |||||
1551 GGAAGAGTTGAGAGTGCCATTTGGCAACTGCGCAAGCTTATGTAGCTGTTAATGATAGT 1610
516 GlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheVal 535
537 |||||
1611 GGGTACCATTCAACTTAACAGTCACGTGGTTACATCATCGCAGTGTGGAGCTTTTGT 1670
536 IleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHis 555
557 |||||
1671 ATCAACACACATCGAGATTTGAGTGTCTCCATCCAAATTCACAAGTTACTTCTCTCAT 1730
556 PheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGly 575
577 |||||
1731 TACAAAGACACCATGTTTATAAATGATCTGCAAGCAAGTTTGTATTAAACGCGGTGCT 1790
576 LeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyr 595
597 |||||
1791 CTTATTGAATCGACTCAGTTTCCGCAAGATATGCTATGGAGCTGTCTATCATATAT 1850
596 LysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAla 615
617 |||||
1851 AAGGAATGGAAGTTCCCGATGAACACTCCCTACTATCTCTTAAGAGAGAGTAGCA 1910
616 ValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAla 635
637 |||||
1911 ATTGAGGACTCAGGCTCTCCCATGGAGTTTCGACTTCTAATAAAGATTAACCCCTTGTCT 1970
636 ValAspGlyLeuLysIleTrpSerAlaLysSerTrpValThrGluTyrCysAsnTyr 655
657 |||||
1971 GTTGATGGCTCGAGATTTGGTCACCCATCAAAACATGGGTACAGATTTACTGCTCCCTC 2030
656 TyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGlu 675
677 |||||
2031 TACTACAAGACGACGACGATTCGAATGATGTCTGAGCTCCATCATGTTGGTGAAGAA 2090
676 LeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThr 695
697 |||||
2091 CTCAGAAAAAGGTGCATACAGACAAAGACAGACCATGGTGGCCCAAAATGCAAACT 2150
696 ValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAla 715
717 |||||
2151 TTTTCAGAGTTTAATTTGAATTCATGCCATATCATATGGATTTCTTCAGCCCTTCACGCA 2210
716 AlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSer 735
737 |||||
2211 CGAGTCAATTTTGGCAATACCTTATGGAGGTACGTTCCCAACAGACCAACCAAGC 2270
736 ArgAsnPheMetProGluProGlySerProGluTyrGluLeuLysThrAsnProAsp 755
757 |||||
2271 AGAAGATTCATGCCAGAGTAGGCACTGCAGAGTACAAAGAAAGTTGAATCAAAACCTGAA 2330
756 LysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIle 775
777 |||||
2331 AAGGCTTTCTTAAGAAACAATCAGCTCGCAAAATAGTGGCTCTCTTTGGGCTCTCGATAAT 2390
776 GluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGlu 795
797 |||||
2391 GAATATTGTCAAGCAGCTTCTGACGAGGTCTACTCTCGGCAAGAGCAGCATTTGAG 2450
796 TrpThrLysAspGlnGluProLysSerAlaPheAlaArgPheGlyLysLysLeuSerAsp 815
817 |||||
2451 TGGACATCAGACAAATCTGCAATTTGAAGCTTTGAGAAATTTGGGAAAGAGCTGTTTGA 2510
816 IleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyPro 835
837 |||||
2511 GTTGAGGATAGAATTTATCGAAGGAATCAAGATGTGAATCTTGAAGATTCGAGCTGGGCT 2570
836 VallysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGly 855

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Db 2571 GTCAATATGCTTACACTTGTCTTCCATCGAGTACTGAGGACTCACTGGGAGAGGA 2630
Qy 856 ileProAsnSerValSerile 862
Db 2631 ATTCCACAGTATCTCCATA 2651
RESULT 10
US-10-425-114-7612
; Sequence 7612, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7612
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700675903_FLI
US-10-425-114-7612
Alignment Scores:
Pred. No.: 2,566-300 Length: 2782
Score: 2909.00 Matches: 549
Percent Similarity: 77.48% Conservative: 122
Best Local Similarity: 63.39% Mismatches: 159
Query Match: 64.16% Indels: 36
DB: 17 Gaps: 9
US-10-731-642A-1 (1-862) x US-10-425-114-7612 (1-2782)
Qy 16 GlyLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThr--- 34
Db 36 GGTCTATAGATAAAGGACAGCTGGTGTGATGCCAGAGATGTTGGACGTGATAGC 95
Qy 35 -----AspIleAsnAlaSerValLeuAsp 42
Db 96 GTAACCAGCGTTGGGGGAATTATTGGTCAAGGCTCTCGACTTAGTTGGCTCAACACTCGAT 155
Qy 43 GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuLeuSerSerValAsnAla 62
Db 156 ACTCTTACTGCTCTTGGCGCGATCCCGTGTCTCTCCAGCTTATTAGTGTACCAAGCT 215
Qy 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaLysLeuGluAsnTrpLeu 82
Db 216 GAT---GCCACGGA---AAGGGAAACTTGGAAAGGCTACCTTTTGGAGGTATCAT 269
Qy 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
Db 270 ACTTCATTGCCAACTTTGGGAGCAGCCCAATCTGCATTCAAAATTAATTTGAATGGAT 329
Qy 103 AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122
Db 330 GATGGAGT---GGAATTCCTGGAGCATTTATATCAAGAAATTTATGCAAACTGAGTT 386
Qy 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
Db 367 TTCTCTGTGAGTTGACTCTTGAAGACATTCACCAACCATGGAGCATCCACTTTGTTC 446
Qy 143 AsnSerTrpValTrpProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162
Db 447 AATTCGTGGATTACAAATGCCAAACTCTTCAAAAGTGACCGCATTTTCTTTGCCAACCA 506
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Qy 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182
Db 507 ACATATCTTCCAAGTGAGACACACAGCTCCACTATCAATATATAGAGAAGAAGTTGAT 566
Qy 183 ThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyrAspTrpAla 202
Db 567 AATTTAAGAGGAGATGGAACCTGGAGAACGCAAGTGGGAAGATCTATGATTATGAT 626
Qy 203 TyrTrpAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGly 222
Db 627 GTCTACCAATGATTAGGTGATCCGATTAAGAGTCAAAATCATGCGCGCTCTGTCTTGA 686
Qy 223 GlySerSerGluTyrProTyrProArgArgGlyArgGlyArgGlyProThrLysThr 242
Db 687 GGAATGACACCTTTCTCTATCTCTGAGGGGAGAACTGTGTAGAAACCAACCAAGGAAA 746
Qy 243 AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArg 262
Db 747 GATCCTAATAGTGAGATGAGG-----AGCAATGATGTTTATCTTCCAGA 791
Qy 263 AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerile 282
Db 792 GATGAGGCTTTTGGACACACTTGAAGTCTCTGACTTCTTACTTATGGACTAAATCCGTA 851
Qy 283 ValGlnLeuLeuLeuProGluPheLysAlaLeuPheAsp-----SerThrHisAsnGlu 300
Db 852 TCTCAAAATGTTCTTCCATTTATTCGAATCTGCTTTTGAATTTGAAATTTACACCCCGTAG 911
Qy 301 PheAspSerPheGluAspValLeuLysLeuTyrGluGlyLysLeuProGlnGly 320
Db 912 TTTGATAGCTTTGATGAAGTTTCATGGACTCTTATTCAGCGCGAATTAAGTCCCA----- 965
Qy 321 ProLeuLysAlaIleThrAspSerile-----ProLeuGluIleLeuLys 336
Db 966 -----ACAGATATATATCAGCAAGATTAGTCCACTACCCGCTGCTTAAG 1007
Qy 337 LeuLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGln 356
Db 1008 GAAATCTTCCGAACTGATGGTGAACAGGCCCTTAAGTTTCTCTCTCTAAAGTAAATTCGA 1067
Qy 357 GluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyVal 376
Db 1068 GTGAGTAACTGTCATGCTGACTGATGAAGATTTGCAAGAGAAATGCTTGTGCTGTA 1127
Qy 377 AsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLys 396
Db 1128 AATCCAACTTGTATGCTTGTCTTAAGGATTTCTTCCAGCAAGCAAGCTAGATAGCCAA 1187
Qy 397 IleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly 416
Db 1188 GTCTATGCTGATCATCTAGTCAATTAACCAAGAACACCTAGAGCCCACTTAGAAGGG 1247
Qy 417 LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIle 436
Db 1248 CTCAGTGTAGATGAGCAATTCAAAACAAGAGATTGTTCTTACTTAGATCATCATGACCCA 1307
Qy 437 LeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArg 456
Db 1308 ATCATGTCATATTTGAGCGCAATAAAT---GCAACCTCCACAAAGGCTTATGCTACCAGA 1364
Qy 457 ThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu 476
Db 1365 ACCATCTTTTCTTGAAAAATGACGGAACITTAGGCCACTTGCATAGAGTTGATTTG 1424
Qy 477 ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGln 496
Db 1425 CCACATCTCTCAGGAGATCAATCTGGTCTTTAGTCAAGTTTTTCTGCTGCAGATCAA 1484
Qy 497 GlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGly 516
Db 1485 GGTGTGAAAGTCTTATTTGGCTCTGACAAAGGCTTATGTTGTAAGTACTGCTGTCG 1544
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Qy	517	ValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaLalleGluProPheValle	536
Db	1545	TATCATCAACTTGTCAACCATTTGGTTAAACACATCATGAGTTGTTAGCCATTCATCATATA	1604
Qy	537	AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrlsLeuLeuHisProHisPhe	556
Db	1605	GCAACAAACAGGCATCTCAGTGTGTTCACCCATATTTATAAATCTCTTCACCCCTCACTAT	1664
Qy	557	ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeu	576
Db	1665	CGTGACACCATTAACATAAAATGGCCCTTGCCTGGGTATCATCTGGTTCACACGACGGTGGCGTT	1724
Qy	577	LeuGlnLeuThrValPheProAlaLysTyrsSerMetGluMetSerAlaValValTyrls	596
Db	1725	ATAGAACAAACATTTTGTGGGAGAGTATCTGTGGAATATGCTGCTAGTATTACAG	1784
Qy	597	AspTrpValPheProGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal	616
Db	1785	GATTTGGGTTTTTACAGATCAAGCATTCGCCCTGATCTTATATAAAAGAGAAATGGCAATT	1844
Qy	617	GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrlsProTyrlsAlaVal	636
Db	1845	GAGGATCCATCTGTCGCCCTCATGGCATTTGGCTTGTGTATGAGGACATACCCCTTATGCTGTT	1904
Qy	637	AspGlyLeuIleThrTrpSerAlaIleLysSerTrpValThrGluTyrlsCysAsnTyrls	656
Db	1905	GATGGACTTCAGATATGGGATGCTATCAACACATGGGTCCATGATACGTTTCTTGTGTAC	1964
Qy	657	TyrlsSerAspAlaValGlnLysAspThrGluLeuGlnAlaThrTrpTyrlsGluLeu	676
Db	1965	TACAAATTCAGATGACACATCTAGAGAAAGATCCTGAATCCCAAGCCTGCTGGAAAGAACTC	2024
Qy	677	ArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrVal	696
Db	2025	GTAGAGTGGGTATGGAGACAGAAATATGAGCCATGGTGGCTTAAGATGCAAACTCGT	2084
Qy	697	GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaA	716
Db	2085	GAAGAGCTAGTTGAAGCTCGCTATCATCATATGGAGCTGCTTCAGCACATTCATGCAGCT	2144
Qy	717	ValAsnPheGlyGlnTyrlsProTyrlsAlaGlyTyrlsLeuProAsnArgProThrLeuSerArg	736
Db	2145	GTAAATTTTGGACAGTATCCCTATGGAGGTTTTTAATCTTAAACCGTCCAACTCTTAGTAGG	2204
Qy	737	AsnPheMetProGluProGlySerProGluTyrlsGluGluLeuLysThrAsnProAspLys	756
Db	2205	CGATTCATGCTCAGAAAGGTTCTGCTGAGTATGAGGNGCTGAGGAAGATCCCGAGAAG	2264
Qy	757	ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu	776
Db	2265	GCTTACTTGAAGACTATTACACCAAAAGTTTCAGACCCCTTATTACCTTTCTGTTATAGAA	2324
Qy	777	IleLeuSerArgHisSerSerAspThrLeuTyrlsLeuGlyGlnArgGluSerProGluTrp	796
Db	2325	ATCTGTGACGGCATGCTATGATGAGGTGTACCTGGGAGAGGAGCAATCAAAATGG	2384
Qy	797	ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle	816
Db	2385	ACATCTGATCAACAGGCATTAGAGGCTTTTAAAGGTTTGGAAATAAACTGGCACAAATT	2444
Qy	817	GluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProVal	836
Db	2445	GAGAAATAAACTCTCAGAGAGAAACACGATGAGAAATCGAGAAACCGTTGTGGACAGATT	2504
Qy	837	LysValProTyrlsThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle	856
Db	2505	CAAAATGCTTATACTCTGCTTTTGGCTTCTAGTAAGGAGGATTAATCTTCAGAGGAATT	2564
Qy	857	ProAsnSerValSerIle	862
Db	2565	CCCAACAGTATCTCTATC	2582

RESULT 11

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US-10-425-114-9323
; Sequence 9323, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9323
; LENGTH: 2804
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700842448_FLI
US-10-425-114-9323

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QY 203 TyrTyrAsnAspLeuGluAspProAspLysGlyGlnAspLeuSerArgProValIleuGly 222
DB 649 GTCTACAATGATTAGGTGATCCGGATAAAGGTGAATCATATGCCCTCGCTGTTCTTGGG 708
QY 223 GlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThr 242
DB 709 GGAATGACACCTTTCCTTATCTCTGCTAGGGGAGAACTGGTAGAANAACCAACGAAGAA 768
QY 243 AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArg 262
DB 769 GATCTAATAGTGAGATAGG-----AGCAATGATGTTTATCTTCCAAGA 813
QY 263 AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle 282
DB 814 GATGAGGCTTTGGACACTTGAAGTCATCTGACTTCTTACTTTATGAGCAATAATCCCGTA 873
QY 283 ValGlnLeuLeuProGluPheLysAlaLeuPheAsp-----SerThrHisAsnGlu 300
DB 874 TCTCAAAATGTTCTCCATTATTGCAATCTGCTTTTGAATTTCAACCCCGTGGAG 933
QY 301 PheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuProGlnGly 320
DB 934 TTTGATAGCTTTGATGAAGTTTCATGCACTCTATTTCAGCGCGAATTAAGCTGCCA----- 987
QY 321 ProLeuLeuLysAlaIleThrAspSerIle-----ProLeuGluIleLeuLys 336
DB 988 -----ACAGATATAATCAGCAAGATTAGTCCACTACCCGCTGCTTAAG 1029
QY 337 GluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGln 356
DB 1030 GAAATCTCCGAACTGATGGTGAACAGGCCCTTAAGTTTCTCTCTTAAGTAATTCAA 1089
QY 357 GluAspLysThrAlaTyrArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyVal 376
DB 1090 GTGAGTAAGTCTGCTGATGATGCTGATGAAGAATTTGCAAGAGAAATGCTTGTGCTGTA 1149
QY 377 AsnProValIleLeuSerArgLeuGlnGluPheProProLysSerLysLeuAspProLys 396
DB 1150 AATCCAAACTTGATTCGTTGCTTAAGGATTTCCCTCCAGCAAGCAAGCTAGATAGCCAA 1209
QY 397 IleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly 416
DB 1210 GTCTATGGTATCATACTAGTCAATATACCAAGAACACCTTAGAGCCCACTTAGAAGG 1269
QY 417 LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIle 436
DB 1270 CTCACCTGTAGATGAGGCAATTCAAACAAAGAGATTGTTCTACTAGATCATCATGCCCA 1329
QY 437 LeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArg 456
DB 1330 ATCATGCCATATTGAGGCGAATAAAT---GCAACCTCCCAAAAGGCTTATGCTACCCAGA 1386
QY 457 ThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu 476
DB 1387 ACCATCTTTCCTGAAAAATGACGGAACCTTAAGGCCACTTGGCCATAGAGTTGAGTTG 1446
QY 477 ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGln 496
DB 1447 CCACATCTCTCAGGAGATCAATCTGCTGCTTTTAGTCAAGTTTCTGCTGCTGCAGATGAA 1506
QY 497 GlyValGluGlySerIleTyrGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGly 516
DB 1507 GGTGTTGAAAGTTCATTATTTGGCTGTAGCAAAAGGCTTATGTTAGTTGAACTGCTGTCG 1566
QY 517 ValHisGlnLeuIleSerHisIleThrLeuAsnThrHisAlaAlaIleGluProPheValIle 536
DB 1567 TATCATCACTTGTGAGCACTTGGTTAAACACTCATGCACTGTTGAGCCATTTCATCATA 1626
QY 537 AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPhe 556
DB 1627 GCAACAAACAGGCATCTCAGTGTGTTTCAACCTTATTTATAAACTCCTTCAACCTCCTAT 1686

QY 557 ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeu 576
DB 1587 CGTGACCACTGACATAAATGGCTTGGCTTATCACTGGTCAACGACGGTGGCGTT 1746
QY 577 LeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLys 596
DB 1747 ATAGAAACAAACATTTTGTGGGAAGGTATTCTCTGGAAATGTCTGTGTAGTTTACAAG 1806
QY 597 AspTyrValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616
DB 1807 GATTGGGTTTTTACAGATCAAGCATTCCTGCTCATCTTATAAAAGAGGAATGGCAAT 1866
QY 617 GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636
DB 1867 GAGATCCATCGTCCCTCATGGCATTCGCCTTGTGATAGAGACTACCTTATGCTGTT 1926
QY 637 AspGlyLeuLysIleTyrSerAlaIleLysSerTyrValThrGluTyrCysAsnTyrTyr 656
DB 1927 GATGGACTTGAGATATGGGATGCTATCAAGACATGGGTCCATGAATAGTTTCTTGTAC 1986
QY 657 TyrLysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTyrTyrLysGluLeu 676
DB 1987 TACAAATCAGATGACACACTTAGAGAGATCCTGAACCTCCAAGCCTGCTGAAAGAACTC 2046
QY 677 ArgGluGluGlyHisGlyAspLysAspGluProTyrProLysMetGlnThrVal 696
DB 2047 GTAGAGGTGGTTCATGGAGACAGANAATGAGCCATGTGGCTTAAGATGCAACTCGT 2106
QY 697 GlnGluLeuIleAspSerCysThrIleThrIleTyrPheAlaSerAlaLeuHisAlaVal 716
DB 2107 GAAGAGCTAGTTGAAGCTTGGCTTATCATCATATGAGCTGCTTCAGCACTTCATGAGCT 2166
QY 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736
DB 2167 GTTAATTTTGACAGATATCCCTATGGAGGTTAATCTTAAACCCGTCACACTCTTAGTAGG 2226
QY 737 AsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLys 756
DB 2227 CGATTATGCTTGAGAAAGGTTCTGCTGAGTATGAGGAGCTGAGGAAGAATCCCCAGAAG 2286
QY 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776
DB 2287 GCTTACTTGAAGACTATTACACCAAGTTTCAGACCCCTTATTGACCTTCTGTATTAGAA 2346
QY 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyr 796
DB 2347 ATCTGTCAAGGCATGCACTGTAGTGAGGTACCTTGGGGAGAGGCAATCCCAATTTGG 2406
QY 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle 816
DB 2407 ACATCTGATCAAGAGCATTAGAGGCTTTTAAAGGTTTGGAAATAAATGGCACAAAT 2466
QY 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProVal 836
DB 2467 GAGAATAAATCTCAGAGAGAAACAAACGATGAGAAACCTGAGAAACCGTTGTGGACAGTT 2526
QY 837 LysValProTyrThrLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856
DB 2527 CAATGCTTATATCTGCTTTCCTTCTAGTAAAGGAAGGATTAACTTTCAGAGGAAT 2586
QY 857 ProAsnSerValSerIle 862
DB 2587 CCCAACAGTATCTCTATC 2604

RESULT 12

US-10-425-114-6926
; Sequence 6926, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack B
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 6926
 ; LENGTH: 2868
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700605994_FLI
 US-10-425-114-6926

Alignment Scores:
 Pred. No.: 2,686-300 Length: 2868
 Score: 2909.00 Matches: 549
 Percent Similarity: 77.48% Conservative: 122
 Best Local Similarity: 63.39% Mismatches: 159
 Query Match: 64.16% Indels: 36
 DB: 17 Gaps: 9

US-10-731-642A-1 (1-862) x US-10-425-114-6926 (1-2868)

QY 16 GlyLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThr--- 34
 DB 135 GGTATAGATAAAGGACAGTGTGTGATCGCGCAAGATGTGTGGACGTGAATAGC 194
 QY 35 -----AspIleAsnAlaSerValLeuAsp 42
 DB 195 GTAACAGCGTTGGGGAATTATTGTCAGAGTCTCGACTTAGTTGGCTCAACACTCGAT 254
 QY 43 GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuLeuLeuSerValAsnAla 62
 DB 255 ACTCTACTGCTTCTGGCGCGATCCGTGTCTCTCCAGCTTATTAGTGTACCAAGCT 314
 QY 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyLeuGluAsnTrpLeu 82
 DB 315 GAT---GCCAACGGA---AAGGGAAACTTGGAAAGGCTTACCTTTTGGAGGTATCATTT 368
 QY 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
 DB 369 ACTTCATTGCCAATCTTGGGACGAGCAATCTGCATTCAAAATTAATTTGAATGGAT 428
 QY 103 AspGluGluPheGlyValProGlyAlaPheIleLysAsnLeuHisPheSerGluPhe 122
 DB 429 GATGGAGT---GGAATCTCTGGAGCATTTATATCAAGAAATTTTATGCAAACTGAGTTT 485
 QY 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
 DB 486 TTCTTTGTGAGTTGACTCTTGAACATCTCAAAACCATGGAGCATCCACTTTGTTGTC 545
 QY 143 AsnSerTrpValTyProAlaAsnLysTyLysSerAspArgIlePhePheAlaAsnGln 162
 DB 546 AATTCGTGATTTACAATGCCAACTCTCAAAAGTGACCGCATTTTCTTGGCCACACAG 605
 QY 163 AlaTyLeuProSerGluThrProAspThrLeuArgLysTyArgGluAsnGluLeuVal 182
 DB 606 ACATATCTTCCAAGTGAGACACACGCTCCACTAGTCAAAATATAGAGAAGAGTTGCAT 665
 QY 183 ThrLeuArgGlyAspGlyThrGlyLysLeuGluTyTrpAspArgValTyAspTyAla 202
 DB 666 AATTAAAGAGGAGATGGAACTTGGAAACGCAAGAGTGGGAAGGATCTATGATTATCAT 725
 QY 203 TyTrpAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGly 222
 DB 726 GTCTACATGATTAGGTGATCCGATAAAGTGAATATCATGCGCCCTCTGTTCTTGA 785
 QY 223 GlySerSerGluTyProTyProArgArgGlyArgThrGlyArgLysProThrLysThr 242
 DB 786 GGAATATGACACCTTTCTCTTATCTCTGTTAGGGGAGAACTGTGTAGAAAACCAACAGGAA 845

QY 243 AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyValProArg 262
 DB 846 GATCTTAATAGTAGAGTAGG-----AGCAATGATGTTTATCTTCAAGA 890
 QY 263 AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle 282
 DB 891 GATGAGGCTTTTGGACACTTGAAGTCATCTGACTTCTTACTTATGAGCTAAATCCGTA 950
 QY 283 ValGlnLeuLeuProGluPheLysAlaLeuPheAsp-----SerThrHisAsnGlu 300
 DB 951 TCTCAAAATGTTCTTCCATTATTGCAATCTGCTTTGATTTGAATTTTCCACCCCGTAG 1010
 QY 301 PheAspSerPheGluAspValLeuLysLeuTyArgGlyGlyIleLysLeuProGlnGly 320
 DB 1011 TTTGATAGCTTTGATGAAGTTCATGCACTCTATTTCAGCGGGAATTAAGTGCCA----- 1064
 QY 321 ProLeuLysAlaIleThrAspSerIle-----ProLeuGluIleLys 336
 DB 1065 -----ACAGATATAATCAGCAAGATTAGTCCACTACCCGCTGCTTAAG 1106
 QY 337 GluLeuLeuArgSerAspGlyGluClyLeuPheLysTyProThrProGlnValIleGln 356
 DB 1107 GAAATCTTCCGAACCTGATGGTGAACAGGCCCTTAAGTTTCTCTCTCTTAAAGTAATTCAA 1166
 QY 357 GluAspLysThrAlaIleArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyVal 376
 DB 1167 GTGAGTAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1226
 QY 377 AsnProValIleIleSerArgLeuGlnGluPheProLysSerLysLeuAspProLys 396
 DB 1227 AATCAAACTTGAATTCGTGTCTTAAGGATTTCCCTCCACGAAGCAAGCTAGATAGCCAA 1286
 QY 397 IleTyGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly 416
 DB 1287 GTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1346
 QY 417 LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIle 436
 DB 1347 CTCAGTAGATGAGCAATTCAAACCAAGAGATTTGTTCTCTAGATGATGATGATGATGATGAT 1406
 QY 437 LeuMetProTyLeuArgArgIleAsnThrSerThrAspThrLysThrTyAlaSerArg 456
 DB 1407 ATCATGCCATATTGAGCGAATAAAT---GCAACCTCCACAAAGGCTTATGCTACCAGA 1463
 QY 457 ThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu 476
 DB 1464 ACCATCTCTTTCTGAAAAATGACGGAACCTTAAAGGCCACTTGCATAGAGTTGAGTTTG 1523
 QY 477 ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyThrProAlaAspGln 496
 DB 1524 CCATCTCTAGGAGATCAATCTGGTCTTTTAGTCAAGTTTCTGCTGCTGCAATGNA 1583
 QY 497 GlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyAlaAlaValAsnAspSerGly 516
 DB 1584 GGTGTGAAGTCTTATTTGGCTGTAGCAAGGCTTATGATGATGATGATGATGATGATGATGAT 1643
 QY 517 ValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaIleGluProPheValIle 536
 DB 1644 TATCATCAACTTGTGAGCCATTGGTTAAACACTCATGCAAGTTGTTGAGCCATTTCATATA 1703
 QY 537 AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyLysLeuLeuHisProHisPhe 556
 DB 1704 GCAACAAACAGCATCTCAGTGTGTTGTTCCCTATTATAAACTCTTCCCTCACCTCATCAT 1763
 QY 557 ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeu 576
 DB 1764 CGTGACCATGAACATAAATGGCTTGTCTGCTGTTATCATCTGGTCAACGACGGTGGCGTT 1823
 QY 577 LeuGluLeuThrValPheProAlaLysTySerMetGluMetSerAlaValValTyLys 596
 DB 1824 ATAGAACAAACATTTTGTGGGGAGGATTTCTGTGGAATGTCTGCTGTGTAGTTTACAAG 1883

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Qy 597 AspTyrValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616
Db 1884 GATTGGGTTTTACAGATCAAGCATGCTGCTGATCTTTATAAAAGAGGAATGGCAATT 1943
Qy 617 GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636
Db 1944 GAGGATCCATCGTGCCTCATGGCATTCGCTTGTGATAGAGGACTACCCCTATGCTGTT 2003
Qy 637 AspGlyLeuLysIleTyrSerAlaIleLysSerTyrValThrGluTyrCysAsnTyrTyr 656
Db 2004 GATGACCTTGAGATGGGATGGCTATCAAGATCGGGTCCATGAATAGCTTTCTTGATC 2063
Qy 657 TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTyrTyrLysGluLeu 676
Db 2064 TACAATCAGATGACACATTAGAAGATCCTGNACTCCAGCTGCTGGAAAGACTC 2123
Qy 677 ArgGluGlyHisGlyAspLysAspGluProTyrTyrProLysMetGlnThrVal 696
Db 2124 GTAGAGGTGGGTGATGGAGATGGCTATCAAGATCGGGTCCATGAATAGCTTTCTTGATC 2063
Qy 697 GlnGluLeuIleAspSerCysThrIleThrIleTyrPheAlaSerAlaLeuHisAla 716
Db 2184 GAAGAGCTAGTGGAGCTGGCTATCATATGAGCTGCTTCAAGCACTTCATGCACT 2243
Qy 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736
Db 2244 GTTAATTTGACAGATATCCCTATGGAGGTTTAATCTTAACCCGTCCAACTCTTAGTAGG 2303
Qy 737 AsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLys 756
Db 2304 CGAATTCATCGCTGAGAAAGGTTCTGCTGATGATGAGGAGCTGAGGAAGATCCCAAG 2363
Qy 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776
Db 2364 GCTTACTTGAAGACTATTACACCAAGGTTTTCAGACCCCTATTGACCTTCTGTTATAGAA 2423
Qy 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyr 796
Db 2424 ATCTTGTCAGGCATGATCTGATGAGCTGTACCTTGGGAGAGGACCAATCCAAATGG 2483
Qy 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle 816
Db 2484 ACATCTGATACAAGAGCATTAAGAGCTTTTAAAGGTTTGGAAATATAACTGGCACAAT 2543
Qy 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProVal 836
Db 2544 GAGATAAAGCTCTCAGAGAGAAACACGATGAGAAACTGAGAAACCGTTGTGGACCAATT 2603
Qy 837 LysValProTyrThrLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856
Db 2604 CAAATGCCTTATCTCTGCTTTTGGCTTCTAGTAGGAAGGATTAACTTTTCAGAGGAAT 2663
Qy 857 ProAsnSerValSerIle 862
Db 2664 CCCAACAGTATCTCTATC 2681
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RESULT 13

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US-10-424-599-73134
; Sequence 73134, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 73134
; LENGTH: 2940
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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37056C.1
US-10-424-599-73134
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Alignment Scores:
Pred. No.: 2,79e-300 Length: 2940
Score: 2909.00 Matches: 549
Percent Similarity: 77.48% Conservative: 122
Best Local Similarity: 63.39% Mismatches: 159
Query Match: 64.16% Indels: 36
DB: 17 Gaps: 9
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US-10-731-642A-1 (1-862) x US-10-424-599-73134 (1-2940)

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Qy 16 GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThr--- 34
Db 135 GGTCAATAGATAAAAGGAGCAGTGTGTGATGCGCAAGAAATGTGTGGACGTGAATAGC 194
Qy 35 -----AspIleAsnAlaSerValLeuAsp 42
Db 195 GTAACACGCGTTGGGGAAATTATTGGTCAAGGCTCGACCTTAGTTGGCTCAACTCGAT 254
Qy 43 GlyValLeuGluPheLeuGlyArgValSerLeuLeuLeuLeuSerSerValAsnAla 62
Db 255 ACTCTTACTGCTTCTTGGGCGGATCCGTGCTCTCTCCAGCTTATTAGTGTACCAAGCT 314
Qy 63 AspProAlaGlnGlyLeuGlnGlyLysArgSerLysAlaIleTyrLeuGluAsnTrpLeu 82
Db 315 GAT---GCCAACGGA---AAAGGGAAACTTGGAAAGGCTACCTTTTGGAAAGGTATCAAT 368
Qy 83 ThrAsnSerThrProIleAlaGlyGluSerAlaPheArgValThrPheAspTyrAsp 102
Db 369 ACTTCATGGCAACTTGGGAGCAGGCCAATCTGCATTCATAAATAATTTTGAATGGAT 428
Qy 103 AspGluGluPheGlyValProGlyAlaPheIleLysAsnLeuHisPheSerGluPhe 122
Db 429 GATGGAGT---GCAATTCCTGGAGCAATTTATATCAAGAAATTTTATGCAAACTGAGTT 485
Qy 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
Db 486 TTCCTGTGTGATTTGACTCTTGAAGACATTCCAAACCATGGAAGCATCCACTTTGTTTGC 545
Qy 143 AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162
Db 546 AATTCGTGGATTTACAATGCCAAACTCTTCAAAGTGCACCATTTCTTCCCAACCCAG 605
Qy 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182
Db 606 ACATATCTTCCAAGTAGACACACAGCTCCACTAGTCAAATATAGAGAAGAGATGTCAT 665
Qy 183 ThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTyrAspArgValTyrAspTyrAla 202
Db 666 AATTAAAGAGGAGATGGAACCTGGAGACGCAAGAGTGGGAAGAGATCTATGATTATGAT 725
Qy 203 TyrTrpAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGly 222
Db 726 GTCTACAAATGATTTAGGTGATCCCGATAAGGTGAAATCATGCCCCTCTGTTCTTGA 785
Qy 223 GlySerSerGluTyrProTyrProArgGlyArgThrGlyArgLysProThrLysThr 242
Db 786 GGAATAGACACTTTCCTTATCTCTGTTAGGGGAGAACTGGTAGAAAAACCAACAGAAA 845
Qy 243 AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArg 262
Db 846 GATCCTAATAGTAGAGTAGG---AGCAATGATGTTTATCTTCCCAAGA 890
Qy 263 AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle 282
Db 891 GATGAGGCTTTGGACACCTGAGTCACTGACCTTCTTACTTATGAGCTAAATCCGTA 950
Qy 283 ValGlnLeuLeuProGluPheLysAlaLeuPheAsp-----SerThrHisAsnGlu 300
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Db 951 TCTCAAAATGTTCTTCATTAATGCAATCTGCTTTTGAATTTACACCCCGTGAG 1010
Qy 301 PheAspSerPheGluaspValLeuLysLeuTyArgGlyGlyLeuLysLeuProGlnGly 320
Db 1011 TTGATAGCTTTGATGAAGTTTCATGACCTTAATTCAGGCGGAATTAAGCTGCCA 1064
Qy 321 ProLeuLeuLysAlaIleThrAspSerIle-----ProLeuGluIleLeuLys 336
Db 1065 -----ACAGATATAATCAGCAAGATTAGTCCACTACCCGTGCTTAAG 1106
Qy 337 GluLeuLeuArgSerAspGlyGlyGlyLeuPheLysTyProThrProGlnValIleGln 356
Db 1107 GAAATCTCCGAACCTGATGCTGAACAGGCCCTTAAGTTCTCTCCTAAAGTAATCAA 1166
Qy 357 GluAspLysThrAlaIleThrArgThrAspGluGlyPheGlyArgGluMetLeuAlaVal 376
Db 1167 GTGAGTAAGCTGCGATGATGCTGATGAAGAATTTGCAAGAGAATGCTTCTGCTGTA 1226
Qy 377 AsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLys 396
Db 1227 AATCCAACTGATTCGTTGCTTAAGGATTTCCCTCCACAGCAAGCTAGATAGCCAA 1286
Qy 397 IleTyArgLysGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly 416
Db 1287 GTCTATGTTGATCATACTAGTCAATAACCAAGAACACCTAGAGCCCACTTAGAAGGG 1346
Qy 417 LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIle 436
Db 1347 CTCACGTGATAGTGAGGCAATTCAAACCAAGAGATTGTTCTCTACTAGATCATCATGCCA 1406
Qy 437 LeuMetProTyLeuArgArgIleAsnThrSerThrAspThrLysThrTyAlaSerArg 456
Db 1407 ATCATGCCATATTTGAGGCGAATTAAT---GCACCTCCAAAGGCTTATGCTACCAGA 1463
Qy 457 ThrLeuLeuPheLeuGlnAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu 476
Db 1464 ACCATCTCTTCTCGAATAATGACGCACTTTAAGGCCACTTGGCCATAGATTGAGTTG 1523
Qy 477 ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyThrProAlaAspGln 496
Db 1524 CCACATCTCCAGGAGATCAATCTCGTGCTTTTGTAGTCAAGTTTCTGCTGCGCATGAA 1583
Qy 497 GlyValGluGlySerIleTyProGlnLeuAlaLysAlaTyAlaAlaValAsnAspSerGly 516
Db 1584 CGTGTGTAAGTTCTATTTGGCTGTAGCAAGGCTTAATGATGTTGTGAATGACTCGTGC 1643
Qy 517 ValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIle 536
Db 1644 TATCATCAACTTGTGAGCCATTTGTTAAACACTCATGTCAGTGTGTTGAGCCATTTCATA 1703
Qy 537 AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyLysLeuLeuHisProHisPhe 556
Db 1704 GCAACAAACAGGCATCTCAGTGTGTTTCACCCCTATTATTAATACTCTCTCACCCCTCACT 1763
Qy 557 ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeu 576
Db 1764 CGTGACCATGACATAAATGCGCTTGTCTCGTTATCACTGTCAACAGCCGTGCGGT 1823
Qy 577 LeuGluLeuThrValPheProAlaLysTySerMetGluMetSerAlaValValTyLys 596
Db 1824 ATAGAACAACATTTTGTGGGGAAGTATTCTGTGGAATATGCTGCTAGTTTACAG 1883
Qy 597 AspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616
Db 1884 GATTGGGTTTTACAGATCAAGCTTGCCTGCTGATCTTTATATAAAGAGGAATGGCAATT 1943
Qy 617 GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyProTyAlaVal 636
Db 1944 GAGGATCCATCTGCGCTCATGGCAATTCGCTTGTGATAGGACTTACCCCTTATGCTGT 2003
Qy 637 AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyCysAsnTyTrp 656

Db 2004 GATGACTTGGATATGGGATGCTATCAAGACATGGGTCCATGAATACGCTTTTCTGTATC 2063
Qy 657 TyLysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu 676
Db 2064 TACAATCAGATGACACACTTAGAAGATCTCTGAAGCTTCAAGCCCTGCTGGAAAGAACTC 2123
Qy 677 ArgGluGluGlyHisGlyAspLysAspGluProTyTrpTrpProLysMetGlnThrVal 696
Db 2124 GTAGAGGTGGGTCTATGGAGACAAAGAAATGAGCCATGGTGGCCCTAAGATGCAACTCT 2183
Qy 697 GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAla 716
Db 2184 GAAGAGCTAGTTGAAGCTTGGCTATCATCATATGAGCTGCTTTCAGCACTTTCATGCGCT 2243
Qy 717 ValAsnPheGlyGlnTyProTyAlaGlyTyLeuProAsnArgProThrLeuSerArg 736
Db 2244 GTTAATTTTGACAGATATCCCTATGAGGTTTAACTTAAACCGTCCAACTCTTAGTAGG 2303
Qy 737 AsnPheMetProGluProGlySerProGluTyArgGluLeuLysThrAsnProAspLys 756
Db 2304 CGATTCATGCTGAGAAAGTTCTCTGATGATGAGGAGCTGAGGAAGATCCCCAGAAG 2363
Qy 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776
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Qy 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLeuSerAspIle 816
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Qy 837 LysValProTyThrLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856
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RESULT 14
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; Sequence 8087, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8087
; LENGTH: 2704
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700733503_FLI
US-10-425-114-8087
Alignment Scores: 5.76e-294 Length: 2704
Pred. No.:

Score: 2849.50 Matches: 535
Percent Similarity: 77.02% Conservative: 122
Best Local Similarity: 62.72% Mismatches: 155
Query Match: 62.85% Indels: 41
DB: 17 Gaps: 9

US-10-731-642A-1 (1-862) x US-10-425-114-8087 (1-2704)

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QY 36 IleAsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGlu 55
DB 111 GTAACCAGC-----GTTGGGGGAATTAAT----- 134
QY 56 LeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerIysAla 75
DB 135 -----GGTCAAGCCCAACGGA---AAAGGNAACCTTGGAAAGGCT 170
QY 76 AlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyLysAlaPhe 95
DB 171 ACCTTTTTGGAGGTATCATTTACTTTCATTCGCCAATTTGGGAGCAGGCCAATCTGCATTC 230
QY 96 ArgValThrPheAspTrpAspGluGluPheGlyValProGlyAlaPheIleIleLys 115
DB 231 AAATAATTTTGAATGGATGATGGAGT---GGAAATCTCTGGAGCAATTTATATCAAG 287
QY 116 AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis 135
DB 288 AATTTATGCAAACTGAGTTTCTCTGTGAGTTTGACTCTTGAAGACATTTCCAAACCAT 347
QY 136 GlyIysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAsp 155
DB 348 GGAAGCATCCCACTTTGTTTGAATTCGTGGATTTTACAAATGCCAACTCTTCANAAAGTGAC 407
QY 156 ArgIlePhePheAlaAsnGluAlaTyrLeuProSerGluThrProAspThrLeuArgLys 175
DB 408 CGCATTTTCTTGGCCACACACATATCTTCNAGTGAGACACCCNGCTCCACTAGTCANA 467
QY 176 TyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTrp 195
DB 468 TATAGAGAAGAAGAGTTGCATAAATTAAGAGAGATGGAACCTGGAGAAGCCAAAGAGTGG 527
QY 196 AspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyLys 215
DB 528 GAAAGGATCTATGATATATGATGTCTACAAATGATTTAGTGATCCCGATTAAGGTGAAAAAT 587
QY 216 LeuSerArgProValLeuGlyLysSerSerGluTyrProTyrProArgArgGlyArgThr 235
DB 588 CATGCCCGTCTGTTCTTGGAGGAATGACACCTTTCTTATCTCTGTTAGGGGNGAAT 647
QY 236 GlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSer 255
DB 648 GGTAGAAAACCAACCAAGAAAGATCCTAATAGTAGAGAGTAGG-----AGC 692
QY 256 LeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeu 275
DB 693 AATGATGTTTATCTTCCAAAGAGATGAGGCTTTTGGACACTTGAAGTCATCTGACTTTCTT 752
QY 276 ThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAsp 295
DB 753 ACTATGAGCTAATAATCGTATCTCAAAATGTTCTTCCATATTATTCATCTGCTTTTAT 812
QY 296 -----SerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGly 313
DB 813 TTGAATTTTACACCCCGTGGTGTGATAGCTTTGATGAAGTTTCATGGACTCTATTTCAGGC 872
QY 314 GlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIle----- 330
DB 873 GGAATTAAGTGGCCA-----ACAGATATATCAAGCAAGATT 908
QY 331 ---ProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyr 349

DB 909 AGTCCACTACCGTGTAAAGAAATCTTCGAACATGATGTGAAACAGGCCCTTAAAGTTT 968
QY 350 ProThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGly 369
DB 969 CCTCCTCTAAAGTAATCAAGTGAAGTCACTGATGATGATGATGATGATGATGATGATGAT 1028
QY 370 ArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGluPheProPro 389
DB 1029 AGAATAATGCTTGTGTTAAATCCAAACTTGAATCGTGTCTTAAAGATTCCTCTCCA 1088
QY 390 LysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGln 409
DB 1089 CGAAGCAAGTAGATGACCAAGTCTATGATGATGATGATGATGATGATGATGATGATGAT 1148
QY 410 IleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPhe 429
DB 1149 CTAGAGCCCAACTTAGAAGGGCTCACTGTAGATGAGGCAATTCAAAACAAGAGATTTGTC 1208
QY 430 IleLeuAsnHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAsp 449
DB 1209 CTACTAGATCATCATGACCCCAATCATGCCATATTTGAGCGCAATTAAT---GCAACCTCC 1265
QY 450 ThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysPro 469
DB 1266 ACAAAGGCTTATGCTACCAGAACCATCTTTCTCGTGAATAATGACGGAACCTTTAAGACCA 1325
QY 470 SerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLys 489
DB 1326 CTTGCCATAGAGTTGAGTTTGCCACATCTCAGGAGATCAATCTGGTGTCTTTAGTCAA 1385
QY 490 ValTyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyr 509
DB 1386 GTTTTCTGCTGAGATGAAGGTGTGAAGTCTATTTGGCTGCTAGCAAGGCTTAT 1445
QY 510 AlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAla 529
DB 1446 GTAGTTGTAATGACTCGTGTATCATCACTTGTGAGCCATGTTGTTAAACACATCATGCA 1505
QY 530 AlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyr 549
DB 1506 GTTCTGAGCCATTCATCATAGCAACCAACAGGATCTCAGTGTGTTCACCCCTATTTAT 1565
QY 550 LysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIle 569
DB 1566 AAATCTCTTCACTCTCATCTGTCGACCAACATGAACATAAATGCGCTTGTCTGTTATCA 1625
QY 570 LeuIleAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGlu 589
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QY 590 MetSerAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeu 609
DB 1686 ATGTCCTGCTGAGTTTCAAGGATTTGGTGTTCACAGATCAAGCATTCGCTGCTGATCTT 1745
QY 610 IleLysArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeuLeuIle 629
DB 1746 ATAAAAGAGAAATGGCAATTCAGATCCATCGTGGCCCTCATGCAATTCGCTTGTGATA 1805
QY 630 GlnAspTyrProTyrAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpVal 649
DB 1806 GAGGACTACCTTATGCTGTTGATGGACTTGAGATATGGGATGCTATCAAGACATGGGTC 1865
QY 650 ThrGluTyrCysAsnTyrTyrLysSerAspAlaValGlnLysAspThrGluLeu 669
DB 1866 CATGAATACGTTTCTTGTACTACAAATCATGACACACTTAGAAGATTCCTGAACTC 1925
QY 670 GlnAlaTrpTrpLysGluLeuArgGluGlyHisGlyAspLysLysAspGluProTrp 689
DB 1926 CAAGCCTGCTGGAAAGAACTCGTAGGGTGTGATGGAGACAGAAATAATGAGCATGG 1985
QY 690 TrpProLysMetGlnThrValGlnGluLeuLeuAspSerCysThrIleTrpIle 709


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Qy 410 IleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPhe 429
Db 1149 CTAGAGCCCACTTAGAAGGGCTCACTAGATAGGCAATTCAAACAAAGAGATTGTT 1208
Qy 430 IleLeuAsnHisHisAspIleLeuMetProTyrLeuArgAlaIleAsnThrSerThrAsp 449
Db 1209 CTACTAGATCATCATGACCAATCATGCAATATTGAGCGCAATAAAT--GCAACCTCC 1265
Qy 450 ThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysPro 469
Db 1266 ACAAGGCTTATGCTACCAAGAACCATCTTTTCTGAAATAATGACGGAACCTTAAGACCA 1325
Qy 470 SerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLys 489
Db 1326 CTGTCATAGAGTTGAGTTGCGCATCTCAGGAGATCAATCTGGTCTTTTAGTCA 1385
Qy 490 ValTyrThrProAlaAspGlnGlyValGluGlySerIleTyrPheLeuAlaLysAlaTyr 509
Db 1386 GTTTTCTGCTGCAGATGAAGTGTGAAGTCTATTGCTGCTAGCAAGGCTTAT 1445
Qy 510 AlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTyrLeuAsnThrHisAla 529
Db 1446 GTAGTTGTGAATGACTCGTGTCTATCATCAACTTGTGAGCCATGTGTTAAACACTCATGCA 1505
Qy 530 AlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyr 549
Db 1506 GTTGTGAGCCATTCATCATAGCAACAACAGGCATCTCAGTGTGTTTCACCCCTATTAT 1565
Qy 550 LysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIle 569
Db 1566 AAATCTTTCACCTTCATCTGACACCATGACATTAATGGCTTGTCTGGTTATCA 1625
Qy 570 LeuIleAsnGlyGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGlu 589
Db 1626 CTGGTCAACGACGGTGGGCTTATAGACAACAACATTTTGTGGGAAGGTAATCTGTGGAA 1685
Qy 590 MetSerAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeu 609
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Qy 610 IleLysArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeuLeuIle 629
Db 1746 ATAAAGAGGAATGGCAATGAGGATCCATCGTCCCTCATGGCATTCGGCTTGTGATA 1805
Qy 630 GlnAspTyrProTyrAlaValAspGlyLeuLysIleTyrSerAlaIleLysSerTrpVal 649
Db 1806 GAGGACTACCCCTTATGCTGTGATGGACTTCAGATATGGGATGCTTATCAAGACATGGGTC 1865
Qy 650 ThrGluTyrCysAsnTyrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeu 669
Db 1866 CATGAATACGTTTCTTGTTACTACAAATCAGATGACACACTTAGAGAAGATCCCTGAAC 1925
Qy 670 GlnAlaTrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrp 689
Db 1926 CAAGCTCTGGAAGAAGACTCGTAGAGTGGGTCAATGGAGACAGAAAATGAGCCATGG 1985
Qy 690 TrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIle 709
Db 1986 TGGCCTAAGATGCAAACTCGTGAAGAGCTAGTTGAAGCTTGGCTATCATCATATGGACT 2045
Qy 710 AlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuPro 729
Db 2046 GCTTCAGACATTCATGACAGCTTTAAATTTTGGACAGATATCCCTATGGAGGTTTAACTTA 2105
Qy 730 AsnArgProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyrGluGlu 749
Db 2106 AACCGTCCCACTCTTAGTAGGGGATTCATGCTGAGAAAGGTTCTGCTGAGTATGAGGAG 2165
Qy 750 LeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGluThrLeu 769
Db 2166 CTGAGGAAGAATCCCCAGAAAGGCTTACTTGAAGACTATTACACCAAGTTTCAGACCCCTT 2225
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Qy 770 LeuGlyIleSerLeuIleGluIleLeuSerArgHisSerAspThrLeuTyrLeuGly 789
Db 2226 ATTGACCTTTCTGTATAGAAATCTTGTCAAGGATGCACTGATGAGGTGTACTTGGG 2285
Qy 790 GlnArgGluSerProGluTyrTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPhe 809
Db 2286 GAGAGGGACAATCCAAATTTGGACATCTGATACAAAGAGCGTTAGAGGCTTTTAAAGGTTT 2345
Qy 810 GlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrp 829
Db 2346 GGAATAAATCGGCACAAATTTGAGATAAATCTCTCAGAGAGAAAACAACGATGAGAAACTG 2405
Qy 830 LysAsnArgSerGlyProValLysValProTyrThrLeuLeuPheProThrSerGluGly 849
Db 2406 AGAAACCGTTGTGGACCAAGTTCAATGCCTTAACTCTGCTTTTGCCTTCTAGTAAGAA 2465
Qy 850 GlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
Db 2466 GGATTAACCTTCAGAGGAATTTCCCAACAGTATCTCTATC 2504
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Search completed: March 14, 2005, 10:53:21
Job time : 1249 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: March 14, 2005, 04:35:30 ; Search time 6629 Seconds
(without alignments)
4949.676 Million cell updates/sec

Title: US-10-731-642A-1
Perfect score: 4534
Sequence: 1 MFLEKIVDAIRGKDDKKVK.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/Cgn2_1/USPTO_spool/US10731642/runat_10032005_102236_5470/app_query.fasta_1.1031
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10731642 @Cgn_1_1_3848@runat_10032005_102236_5470 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2696.5	59.5	3135	AY103567	AY103567 Zea mays
2	2624	57.9	2571	9 CL962567	CL962567 OsIFCC008
3	1874	41.3	2682	9 CL969033	CL969033 OsIFCC017
4	1771	39.1	2857	3 CINS0AARPK	BX816626 Arabidops
5	1743.5	38.5	2928	3 AY110012	AY110012 Zea mays
6	1717.5	37.9	2739	3 AY109573	AY109573 Zea mays
7	1658	36.6	4458	9 CL975314	CL975314 OsIFCC027
8	1509.5	33.3	918	7 CK268592	CK268592 EST714670
9	1462.5	32.3	2643	9 CL979503	CL979503 OsIFCC033

10	1403.5	31.0	2835	9	CL979507	CL979507 OsIFCC033
11	1277.5	28.2	916	7	CK271202	CK271202 EST80
12	1262	27.8	935	7	CK255133	CK255133 EST738770
13	1259.5	27.8	910	7	CV471979	CV471979 45239.1 C
14	1235.5	27.2	983	7	CV472045	CV472045 45315.1 C
15	1233	27.2	1473	3	CNS0AAZ0	BX818403 Arabidops
16	1198	26.4	765	4	BI422183	BI422183 EST532849
17	1189	26.2	882	7	CV471573	CV471573 44757.1 C
18	1188.5	26.2	808	4	BM411588	BM411588 EST585915
19	1186.5	26.2	893	7	CV470308	CV470308 43145.1 C
20	1184	26.1	782	7	COL00713	COL00713 GR_Eb002
21	1182.5	26.0	830	7	CV472049	CV472049 45319.1 C
22	1181	26.0	790	7	CV469947	CV469947 42715.1 C
23	1176	25.9	722	2	AW030773	AW030773 EST274028
24	1170.5	25.8	868	7	COL29962	COL29962 GR_Eb31H
25	1158	25.5	1091	3	CNS0AB1Z	BX818359 Arabidops
26	1156.5	25.5	806	7	CV472057	CV472057 45329.1 C
27	1149.5	25.4	801	7	CV472255	CV472255 45564.1 C
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31	1131	24.9	895	7	CK250792	CK250792 EST734429
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33	1123.5	24.8	775	4	BM412715	BM412715 EST587053
34	1122	24.7	663	4	BG890287	BG890287 EST516138
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37	1113	24.5	791	4	BM411405	BM411405 EST585732
38	1112.5	24.5	752	4	BG593074	BG593074 EST491752
39	1111.5	24.5	728	4	BI423111	BI423111 EST533777
40	1108	24.4	1158	7	CK161284	CK161284 FGAS01385
41	1104.5	24.4	749	4	BM411164	BM411164 EST585491
42	1103	24.3	880	7	CV472589	CV472589 45955.1 C
43	1102	24.3	817	4	BM411179	BM411179 EST585506
44	1102	24.3	841	7	CV470085	CV470085 42879.1 C
45	1101	24.3	774	7	CV471624	CV471624 44818.1 C

ALIGNMENTS

RESULT 1
AY103567
LOCUS Zea mays PC0116252 mRNA sequence. 3135 bp linear HTC 16-OCT-2002
DEFINITION Zea mays PC0116252 mRNA sequence.
ACCESSION AY103567
VERSION AY103567.1 GI:21206645
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 3135)
AUTHORS Hayney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 3135)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
LOCATION/Qualifiers 1. 3135
/organism="Zea mays"

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Qy 243 AspProAsnSerGluSerArgGlyProLeuLeuMetSerLeuAspIleTyrValProArg 262
Db 727 GATCCGAGCTCGAGAGTAGGCTGCTGCTGGTGGAG-----CAGATCTAGCTGCGCGG 780
Qy 263 AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle 282
Db 781 GACGAGCGGTTCGGGCACCTGAAGATGCGGAGCTTCTTGGGCTACTCGATCAAGCGATC 840
Qy 283 ValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAsp 302
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Qy 343 GlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnLysAspLysThrAlaTrp 362
Db 1021 GCGGACTATCTCCTCAAGCTCCCACTGCTCGATATATCAACAGGCAAGGAGCGGTGG 1080
Qy 363 ArgThrAspGluLeuPheGlyArgGluMetLeuAlaGlyValAsnProValIleLeuSer 382
Db 1081 AGGACAGACGAGAGTTCGCGGAGGAGTCTCGCGCGGTGAACCCGATGATGATCAG 1140
Qy 383 ArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsn 402
Db 1141 CGTCTCAGGAATTCCTCCGAAAGTAGTCTCGATCTTAGCAAGTTCGGGACCAACC 1200
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Qy 703 CysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyr 722
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RESULT 3

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LOCUS OsIFCC017680 Oryza sativa Express Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL969033
VERSION CL969033.1 GI:52392695
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoideae; Oryza.

1 (bases 1 to 2682)

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis

Unpublished (2004)

Contact: Chen Chen

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Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559

Fax: 86-10-80488676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

Location/Qualifiers

1..2682

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="genomic DNA"

/db_xref="taxon:39946"

/clone_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences"

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Qy ArgLysProThrLysThrAspProAsnSerGluSerArgLysProLeuLeuMetSerLeu 256
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838 CAC-----GCGAGCGCGAGAGAGGCTGGAG-----TACCGCGAG 873
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Alignment Scores:

Pred. No.: 2,648-192 Length: 2682
Score: 1874.00 Matches: 384
Percent Similarity: 60.33% Conservative: 127
Best Local Similarity: 45.34% Mismatches: 310
Query Match: 41.33% Indels: 26
DB: 9 Gaps: 12

US-10-731-642A-1 (1-862) x CL969033 (1-2682)

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Qy 80 AsnThrLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99
Db 379 GGTGTGTCGACAGAAG-----GAGTCAAGCGGAGCGCGGTGTGTATC 423
Qy 100 AspTrpAsp-----AspGluGluPheGlyValProGlyAlaPheIleLysAsn 116
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RESULT 4
CNSOAAKP
LOCUS
DEFINITION
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH592E11 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).
ACCESSION
BX816626
VERSION
BX816626.1 GI:42469981
KEYWORDS
HTC; GSLT_cDNA.
SOURCE
Arabidopsis thaliana (thale cress)
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ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 2857)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 2857)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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DEFINITION Zea mays CL902_1 mRNA sequence.
ACCESSION AY109573
VERSION AY109573.1 GI:21213344
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 2739)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2739)
AUTHORS Coe,E.H.
DIRECT SUBMISSION
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schubert, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
FEATURES
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Pred. No.: 3.24e-175 Length: 2739
Score: 1717.50 Matches: 360

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 1 (bases 1 to 4458)
 Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
 An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
 Unpublished (2004)
 JOURNAL
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
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 Class: exon-trapped.
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RESULT 8

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LOCUS EST714670 potato abiotic stress cdna library Solanum tuberosum CDNA
DEFINITION clone POACH67 5' end, mRNA sequence.

ACCESSION

CK268592

VERSION

CK268592.1

KEYWORDS

EST.

SOURCE

Solanum tuberosum (potato)

ORGANISM

Solanum tuberosum

REFERENCE

1 (bases 1 to 918)

AUTHORS

Buell C.R., Hart A., Zismann V., Karamycheva, S.A. and Baker, B.

JOURNAL

Unpublished (2003)

COMMENT

Generation of ESTs from abiotic stressed potato tissue

CONTACT

Contact: Robin Buell

INSTITUTION

The Institute for Genomic Research

ADDRESS

9712 Medical Center Dr. Rockville, MD 20850, USA

E-MAIL

Email: potato-array@tigr.org

CLONES

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

Location/Qualifiers

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Qy 288 ProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspVal 307
Db 982 ACGGCC---CAGGGGTGTCCGAGACCGCGCGGAGCTTCCCGTCTGCTGCGCGCGATC 1038
Qy 308 LeuLysLeuTyrGluGlyGlyIleLys---LeuProGlnGlyProLeuLeuLysAlaIle 326
Db 1039 GACGCGCTGTACGAGCGGTGTACAGAACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1095
Qy 327 ThrAspSerIleProLeuGluIleLeuLysGlyLeuLeuArgSerAspGlyGluGlyLeu 346
Db 1096 ---GACAACCTC-----GAGAGTTCAAGGAGGAGCTG-----GAAGGCTAC 1113
Qy 347 PheLysTyrProThrProGlnValIleGlnGlu-----Asp 358
Db 1114 TTCAGG-----GAGGTGCTCCAGAAAGCAGGTAAGCTGCTGCTCGAGGCGGAG 1161
Qy 359 LysThrAlaTyrArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnPro 378
Db 1162 AAG-----GAGAGTTCAAGGAGGAGCTG----- 1185
Qy 379 ValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyr 398
Db 1186 -----CGCAAGACTTCCCTATATTATTCAGCAAGCTCGACGAGGAACCTAC 1230
Qy 399 GlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly---Leu 417
Db 1231 GCGCCAGGGGACTCCCTCATCACGAGAGCTGATTGAAGACGAGATTAATGGGGTCA 1290
Qy 418 ThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIleLeu 437

Db 1291 ACACGAGGAGGCGTGTCTGAACAAGACTATTCTGCTGGACTACACGACATGTT 1350
Qy 438 MetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThr 457
Db 1351 CTGCGGTCTGTCGACCGCGGTGCGGAGCTGAGACACACCGCTGTACGCTCGCGGAG 1410
Qy 458 LeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuPro 477
Db 1411 CTCTTCTTCTGACGAGGAGGCGCGCTGCGCGGATCGCCATCGAGCTGACGAGGCC 1470
Qy 478 ---HisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGln 496
Db 1471 AAGTCCCCCAACACCGCGAGTGG-----CGCAGGTCTTCACGCGCGGACACG 1521
Qy 497 GlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGly 516
Db 1522 GTGCGCGCGTCTGCTGCTGTGCGAGCTGCCAAAACGACGCTCTCGCCACGACACGCG 1581
Qy 517 ValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIle 536
Db 1582 TACCACGAGCTCTGTCAGCACTGCTGAGGAGCGACTGCTCGTGGAACCTGATGATC 1641
Qy 537 AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPhe 556
Db 1642 GCGCGGAACCGCGCGTGGAGCCAGATGCACCCATCTACCGGTCTGTCACCGCACCTTC 1701
Qy 557 ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeu 576
Db 1702 CGCTTTCACCTGGAGATCAACGCCGCGCGCGGATGCTCATCAACGCCCAATGGAATC 1761
Qy 577 LeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValTyr--- 595
Db 1762 ATCAGAGCGCTTCGCGCGCGGGAAGCATGTCATGAGCTCAGCTCGCGGTTCACGAC 1821
Qy 596 LysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAla 615
Db 1822 AAGTTTGGCGATTCGATCGAGGCTCTGCCCGCATCTCATCCGAGGGGCGATGCG 1881
Qy 616 ValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAla 635
Db 1882 ATCGAATCGGAGGATGCGAGCTG-----GAGCTGAGTAGAGGACTACCCGTTACGCC 1935
Qy 636 ValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyr 655
Db 1936 AACGACGCTTACTCTCTGAGCTCCATCAAGAGTGGGTGTGAGACTAGTGNACCAT 1995
Qy 656 TyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGlu 675
Db 1996 TACTACAGTTGGCTTCGACATCCATGACAAAGAGCTCCAGGGTGTGGGAACGAG 2055
Qy 676 LeuArgGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThr 695
Db 2056 GTGCGAAACAGAGGCCACCGGACAAG-----GAGGAAGGCTGCGCAGACTGAACTGC 2109
Qy 696 ValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAla 715
Db 2110 CACGGGAGCTCTGTCGAGGTCTGACCATCATCTGCGGTGCGGTGCGGCGACCATGCG 2169
Qy 716 AlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSer 735
Db 2170 GCGGTGAACCTTCGCGCAGTACCCCTACGCGGGTACTTCCCAATCGCCACCATCGCC 2229
Qy 736 ArgAsnPheMetProGluProGly-----SerProGluTyr 747
Db 2230 CGCGCGAATCATCGCGAGGCGGAGCGCGTGCAGTCACGCGCATGACGCCAACGTT 2289
Qy 748 GluGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGln 767
Db 2290 GTTGA-----GATCCGCTCAGGTGTACTAGACAGTTCCTCCATCGAGTACCAG 2340
Qy 768 ThrLeuLeuGlyIleSerLeuIleGluLeuSerArgHisSerSerAspThrLeuTyr 787

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Db      2341 ACCACCTCGTCTGCGCGTCTCAACCTGCTATCGTCACACTCGCGCGCGAGGAGTAC 2400
Qy      788 LeuGlyGlnArgGluSerProGluTTPThrLysAspGlnGluProLeuSerAlaPheAla 807
Db      2401 ATGGGACCCAGCGGAGTACAGGTGGATGGCGGACAGGAGGTACAGGCGCGTTCGGG 2460
Qy      808 ArgPheGlyLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGlu 827
Db      2461 AGTTCAACGAGGATGATGATATCGCGGAGATCATCGACTCGCGGACAAAGATCCG 2520
Qy      828 LysTrpLysAsnArgSerGlyProValLysValProTyrThrLeuLeuPheProThr--- 846
Db      2521 GAGCGAAAGAACCGCGCGCGCGCGTGTGCGGTACGTGCTCAAGCGCTCTAC 2580
Qy      847 -----SerGluGlyGlyLeuThrGlyLysGlyLysGlyLysProAsnSerValSerIle 862
Db      2581 GGTGACCTTAAGACATGACGTCGCGTGATGGAGATGGGTATCCCCAACGATCTCAATT 2640

RESULT 10
LOCUS   CL979507
DEFINITION OsIFCC033431 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL979507
VERSION  CL979507.1 GI:52413505
KEYWORDS GSS.
SOURCE  Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE 1 (bases 1 to 2635)
AUTHORS  Ma,L.Y., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE    An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL  Unpublished (2004)
COMMENT  Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES             Location/Qualifiers
     source           1..2835
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Alignment Scores:
Pred. No.:      6.2e-141      Length:      2835
Score:          1403.50      Matches:      323
Percent Similarity: 54.14%      Conservative: 115
Best Local Similarity: 39.93%      Mismatches:  274
Query Match:     30.96%      Indels:       97
Db:              9           Gaps:         22

US-10-731-642A-1 (1-862) x CL979507 (1-2835)

Qy      83 ThrAsnSerThrProfile-----AlaAlaGly 91
Db      610 ACATCTCAGTCCATTAGCGCGGACGAGAGAAATTCCTCCGATTAAGGCACGTGAT 669
Qy      92 GluSerAlaPheArgValThrPheAspTrpAspGluGluPheGlyValProGlyAla 111
Db      670 GACTCTCGTCTCTTACTTACTCAAAATGGTGGGACGAGAACTCTCAAGTTTCCGCGCATC 729

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Qy      112 PheIleIleLysAsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAsp 131
Db      730 GTCATAAATCGCCAAAAGAGATGAGGAAGTGTCCAGCTGAAGAAAGTACTTT----- 783
Qy      132 ValProAsnHisGlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLys 151
Db      784 -----GGAGAAGCTACTCGCATTTGTAATTCG----- 810
Qy      152 TyrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAsp 171
Db      811 -----TACCTCCCGTCTCAGACGCCAG 834
Qy      172 ThrLeuArgLysTyrArgGluAsnGlnLeuValThrLeuArgGlyAspGlyThrGlyLys 191
Db      835 GCGGTGAAGAATCTCGCAAGGAAGAGCTCAGGGCCATCCGCGGATGTCGCGCGGAG 894
Qy      192 LeuGluGluTTPAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAsp 211
Db      895 CGCAAGGAGTGGAGCGCATCTACGACTACGACGTCTACAACGACCTCGCGCACCCGAC 954
Qy      212 LysGlyGlnAspLeuSerArgProValLeuGlyLysSerSerGluTyrProTyrProArg 231
Db      955 AATGACCCGCGCACCTCGTCGCGCGTGTCTCGCGCGCGCGCGC---CCCTACCGCGC 1011
Qy      232 ArgGlyArgThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIlePro 251
Db      1012 CGCTCCCGACCGCGCGCGCGCGTGCAGGACAGACCGCTGCTCGGAGTTCGCGC---CCG 1068
Qy      252 LeuLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeu 271
Db      1069 GCCAAGGACGCGCGCGGATCTACGTGCCACGAGCAGGCGTTCACGAGCGGGAAGGCC 1128
Qy      272 SerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLys 291
Db      1129 GCGCGGTTCGCCACCAAGAGCGCTGTCGCGCTGTCTCGGCTTCCACCACGCGCAGAGG 1188
Qy      292 AlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyr 311
Db      1189 GTGTCCGCGACCGCGCGCGGCG---TTCGCGTCTGCGCGGCATCAGCGCTGTATC 1245
Qy      312 GluGlyGlyIleLys---LeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIle 330
Db      1246 GAGGACGGGTACAGAACCGCGCGTCTGTCGCGCAGCAGGAGCGC---GACAACCTC 1299
Qy      331 ProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrPro 350
Db      1300 -----GAAGGCTACTTCAGG----- 1314
Qy      351 ThrProGlnValIleGlnGluAsp---LysThrAlaTTPArgThrAsp---GluGluPhe 368
Db      1315 -----GAGGTGCTCCAGAGCAGGTGAAGCTGTCTCAAGGGGCGAGGAAGGAGGTTC 1368
Qy      369 GlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGluPhePro 388
Db      1369 AAGGAGGAGCTA-----CGCAAGACTTCCCT 1395
Qy      389 ProLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGlu 408
Db      1396 ATATTCAAGAGCTGGACGAGAAACCTACGCGCCCGGAGGACTCTCATCAACCAAGAG 1455
Qy      409 GlnIleGluAspLysLeuAspGly---LeuThrIleAspGluAlaIleLysThrAsnArg 427
Db      1456 CTGATTGAAGAGCAGATTAAATGGGGTCAACAGCAGAGGAGGCGCTGTGAAGAAGAAAG 1515
Qy      428 LeuPheIleLeuAsnHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSer 447
Db      1516 CTGTTTCAGTCTGGACTACACGACGTGCTCTCGCGTTCGTGCACGCGCGTGGCGGAGCTG 1575
Qy      448 ThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAsnGlyThrLeu 467
Db      1576 GACGACACCGCTGTACGCTCGCGGAGCGCTCTTCTTCTTCTGACGAGGACGCGCAGCTG 1635

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Score: 1277.50 Matches: 234
Percent Similarity: 89.22% Conservative: 39
Best Local Similarity: 76.47% Mismatches: 32
Query Match: 28.18% Indels: 1
DB: 7 Gaps: 1

US-10-731-642A-1 (1-862) x CK271202 (1-916)

Qy 355 ileGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAla 374
Dy 2 ATTAAGATTGATAGTCTGCTGAGGACACATGAGAGTTTGACGGAAATCTAGCT 61
Qy 375 GlyValAsnProValIleSerArgLeuGlnGluPheProProLysSerLysLeuAsp 394
Dy 62 GGATGCAACCTGTTATCATTCGACGCTTCCAGAGTTTCCCGGCTAGCAAGTTGGAT 121
Qy 395 ProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeu 414
Dy 122 CCTGAAGTATATGTTATCATGACAGCTTCATCAAAAGGGAGCATAGAGAAAACATG 181
Qy 415 AspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHis 434
Dy 182 GATGGACTAATGATGAGTATTGAGTGTAATAGGCTGTTATTTATGACCATCAT 241
Qy 435 AspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAla 454
Dy 242 GATGCATTGTTGCTTACCTAAGCGGATTAATACA---ACAAAACGAAAGACTTATGCC 298
Qy 455 SerArgThrLeuLeuPheLeuGlnAsnAsnGlyThrLeuLysProSerAlaIleGluLeu 474
Dy 299 AGTCGGACTCTCTCTTTCTTCAGATAATGGAACATTTAGGCGCACCTTGCAATTGAGTTG 358
Qy 475 SerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAla 494
Dy 359 AGCTTACCTCATCCACAGGAGATAACATGTTGCCACCGCTTGTATTACACAGCC 418
Qy 495 AspGlnGlyValGluGlySerIleTyrGlnLeuAlaLysAlaTyrAlaValAsnAsp 514
Dy 419 AACAAAGGTTGTTGAAGGCACTGTCTGGCAGCTGCGCAAGCTTATGCGCTGTAATGAT 478
Qy 515 SerGlyValHisGlnLeuIleSerHisThrLeuAsnThrHisAlaAlaIleGluProPhe 534
Dy 479 TCTGGCTATCATCAGCTTATCAGTCATTTGGTTAAATACTCATGCAACATAGAGCCATTT 538
Qy 535 ValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisPro 554
Dy 539 GTGATTCTACAAATAGACATTTGAGCGTACTTTCATCAATATTCAGCTTTTACACCT 598
Qy 555 HisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGly 574
Dy 599 CATTTCCGTATACCATGATATATAATGCTTTGGCTCGGAGATCTCATCAATGCAAGT 658
Qy 575 GlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValVal 594
Dy 659 GGAATCTTCTGAGTGCAGATTTTCCAGGAGAAATATGCCATGGAATGTCTATTTGTC 718
Qy 595 TyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyVal 614
Dy 719 TATAAAACCTGGGTGTTCTACTGACAGAGGACTTCTCTGCTATCTTCTTAAGAGAGAGTA 778
Qy 615 AlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyr 634
Dy 779 GCAGTGTAGACTCAAGCCAGCCCTATGGCTTAAACTTCTTAATTGAGGATTTATCCTTTT 838
Qy 635 AlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsn 654
Dy 839 GCTGTAGATGGCTTGGAGTTGGGAGCAATCGAAGCCTGGGTGTGACTACTGTCTCA 898
Qy 655 TyrTyrTyrLysSerAsp 660
Dy 899 TTCATTACTCAACTGAT 916

CK255133
LOCUS
DEFINITION
EST738770 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POC186 5' end, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
ORIGIN
Alignment Scores
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-731-642A-1 (1-862) x CK255133 (1-935)
Qy 422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIleLeuMetProTyrLeu 441
Dy 20 GCATCAAGAAAGAGACTGTTTCATTTGGATTCACCATGACGCTTAATGCGTACTTG 79
Qy 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461
Dy 80 AAACGTATATAACACACTACC---ACACAGAGCTATGCTCTCAAGAACATTTGCTTTCTTG 136
Qy 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481
Dy 137 AATGAGATGGATTCATTGAAGCCACTTGTGTTAGTTAACT-----CGAAGAGAT 187
Qy 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501
Dy 188 GAGCAATCGAGAAATTGTTAGCAATGTATATACCCGGAGAACTGGTGCTGAAGCAACC 247
Qy 502 IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521
Dy 248 ATTTGGCAGCTTGCAAAAGCTTATGTACAGTGAATGATTCCTGGGTTTCACACAGCTTGT 307
Qy 522 SerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGln 541
Dy 308 TCTCATTTGTTGCACACTCATGCAGTAACCTGAGCCATTTATCATAGCAACAAACACACAA 367

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QY 542 LeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561
Db 368 TTAAGTGTCTTCATCCCAATTTATAAGCTTTTGACACCTCTCACTCCGCGACCAATGTAC 427
QY 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrVal 581
Db 428 ATTATGCAATTTGGCCCGCTCAATTTCTCATCTGATGCTGATGGAATTTCTAGAATGACAGTT 487
QY 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601
Db 488 TTTCTGCGGAAGTTTCTCTCGGAATGTCTGCAATGTACAGTACCAATTTACAAGGACTGGGTTTCCCT 547
QY 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSer 621
Db 548 CAGCAAGCTTTTGCCTTCCGATCTCATCAAGAGAGGAATGGCTGTGGAGGACTCAAGCCAA 607
QY 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAlaValAspGlyLeuLysIle 641
Db 608 CCACATGGCATCAAGCTAGTTATAGAGGACTATCTCATATGATGATGAGCGGCTCGAGATT 667
QY 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrLysSerAspAsp 661
Db 668 TGGTCTGCAATCAACACATGGGTGAGAGACTACTGCAACTTCTATTACAAAACCGATGAA 727
QY 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHis 681
Db 728 ATGGTCAAGATAGACACAGAACTGCAGTCTTGTGGTGAAGAAGACGCGGGAAGGGGGCAT 787
QY 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701
Db 788 GGAGCAAAAGGAAGAACCATGTGGCTTAGATGCGAGCTCGCGAAGAACTCATAGAT 847
QY 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721
Db 848 TGTTCACCAATCATATATGATGATGCTTTCAGCACTTTCATGCGAGCAATAAATTTTCGGGCAA 907
QY 722 TyrProTyrAlaGlyTyrLeuProAsn 730
Db 908 TATCCTTACGGAGGATACCCCTCCAAAC 934

RESULT 13
CV471979
LOCUS 910 bp mRNA linear EST 01-OCT-2004
DEFINITION 45239.1 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone
45239 5', mRNA sequence.
ACCESSION CV471979
VERSION CV471979.1 GI:53696755
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
REFERENCE 1 (bases 1 to 910)
AUTHORS Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De
Koeber, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
TITLE Generation of ESTs from common scab-challenged potato tubers
JOURNAL Unpublished (2004)
COMMENT Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

FEATURES
Location/Qualifiers
1..910
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/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="45239"
/tissue_type="tubers"
/lab_host="XL10-Gold"

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/clone_lib="Common Scab-Challenged Tubers"

/note="Vector: pBluescript II SK(+); XR; Site 1: EcoRI; Site 2: XhoI; supplier: Pathogen-Challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with Streptomyces scabei EF-35, by applying 1 ml of a spore stock (OD₆₅₀ = 0.7). Tubers were placed in trays of sand and watered from the bottom for the remainder of the experiment. Inoculated tubers were sampled at 2 days, 1 week, 2 weeks and 4 weeks post-infection. Harvested tubers were washed in distilled water, blotted dry, cut into small pieces and frozen in liquid nitrogen. RNA was isolated from each sample collection, pooled and used for cDNA library construction."

ORIGIN

Alignment Scores:	4.93e-126	Length:	910
Pred. No.:	1259, 50	Matches:	243
Score:	91.50%	Conservative:	26
Percent Similarity:	82.65%	Mismatches:	24
Best Local Similarity:	27.78%	Indels:	3
Query Match:	7	Gaps:	1
DB:			

US-10-731-642A-1 (1-862) x CV471979 (1-910)

QY	367	GluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGlu	386
Db	2	GAATTCGACAGAGAAATGCTAGCTGGAGTTAATCCTATCATATATTAGTAGACTTCAAGAA	61
QY	387	PheProProlLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThr	406
Db	62	TTTCTCTCAAAAGCAAGCTAGATCCCGAAGCATATGGAATCAAAACAGTACAAATTA	121
QY	407	ArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThrAsn	426
Db	122	GCAGAACACATAGAGGATAAGCTGGATGGAATAACGGTTGATGAGCGCATGAACAATA	181
QY	427	ArgLeuPheIleLeuAsnHisAspIleLeuMetProTyrLeuArgArgIleAsnThr	446
Db	182	AAACTTTTTCATATTGAACCATCATGATGTAATTATACCATATTTGAGGAGATAAAC	241
QY	447	SerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAsnGlyThr	466
Db	242	---ACAATAACGAAACATATGCTCGAGAACTTTGCTCTTCTTCAAGATAATGGA	298
QY	467	LeuLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAla	486
Db	299	TTGAAGCCCATAGCAATTTGAATTGAGTTTGCACATCCAGATGGAGATCAATTTGGT	358
QY	487	ValSerLysValTyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAla	506
Db	359	ACTAGCAAGTGTATATCTCAAGTGATCAAGGTGTGAGAGCTCTATCTGGCAATTTGG	418
QY	507	LysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeuAsn	526
Db	419	AAAGCTTAATGTTGGTGGAATGACACTGGTGTTCATCACTAATATTAGTCATGTTGA	478
QY	527	ThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHis	546
Db	479	ACTCATGCAGTATCGAGCCATTTGTGATTGCAACAAACAGCAACTTAGTGTGCTTCA	538
QY	547	ProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAla	566
Db	539	CCTATTCATAAGCTTCTATATCTCATTTCCGGGACACAATGAATTAATGCTTCGGCA	598
QY	567	ArgGlnIleLeuIleAsnGlyLeuLeuGluLeuThrValPheProAlaLysTyr	586
Db	599	AGACAAATCTTAGTCAATGCTGGTGGAGTTCTTGAGAGTACAGTTTTTCAATCCAAT	658
QY	587	SerMetGluMetSerAlaValTyrLysAspTrpValPheProGluGlnAlaLeuPro	606
Db	659	GCCATGGAATGTGAGCTGTGTTTACAAAGATTGGGTTTTTCCCTGATCAAGCCCTTCG	718


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VERSION      BX818403.1 GI:42470778
KEYWORDS     HTC; GSLT cDNA.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE    1 (bases 1 to 1473)
AUTHORS      Castellì,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE        Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1473)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
COMMENT      The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castellì
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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             /db_xref="taxon:3702"
             /clone="GSLTSL1772C01"
             /tissue_type="Silique"
             /plasmid="pCMVSPORT_6"
             1..1473
             /gene="At1g17420"
gene
ORIGIN
Alignment Scores:
Pred. No.:      8,46e-123      Length:      1473
Score:          1233.00      Matches:    237
Percent Similarity: 66.60%      Conservative: 92
Best Local Similarity: 47.98%      Mismatches: 158
Query Match:    27.19%      Indels:    7
DB:             3           Gaps:       6

US-10-731-642A-1 (1-862) x CNS0AAZO (1-1473)
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Db      1   CGTCAAGCCATAGCTGGGAATCAATCCAGTGAACATTGAGAGAGTCAAGACTTTTCCACCG 60
Qy      390  LysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGln 409
Db      61  GTCAGCAATCTTGACCCCAAGATCTACGGTCCACAACACTCGCTCTTACTGACGACCAT 120
Qy      410  IleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPhe 429
Db      121  ATCATTGTGTCACCTCGACGGATTCTCCGTACCAACAAGCGTTGGAAGAGAGATAGATTGTAT 180
Qy      430  IleLeuAsnHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAsp 449
Db      181  ATGTTGGATTACCATGACATATCTTACCCTTCTTAGACCGGATTAATTCGCTAGACGGA 240
Qy      450  ThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysPro 469
Db      241  CGCAAAAGCCTATGCTACTCGAAGCTATCTTCTTGTACTCGTCTAGGCACACTTAAGCGC 300
Qy      470  SerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLys 489
Db      301  GTAGCCATTGAGCTAAGCTCCCTC---CCCATGGTCCAAAACATCGGTCC---AAGCGT 354
Qy      490  ValTyrThrProAlaAspGlnGlyValGluGlySerIleTyrGlnLeuAlaValAlaTyr 509
Db      355  GTGCTTACACCTCCAGTCGATCGAACCTCTAATTTGGATGTGGCAGCTCGCTAAAGCCCA 414
Qy      510  AlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisThrLeuAsnThrHisAla 529
Db      415  GTTAGTTCTAACGATGCTGGTGTCCATCAGCTTGTCAATCACTGTTACGGACACATGCA 474
Qy      530  AlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyr 549
Db      475  TGCCTGGAGCCATTATATTAGCTGCACACAGGCAATTAGCGCTATGATCCCATATTC 534
Qy      550  LysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIle 569
Db      535  AAGCTACTGGATCCACATGAGATACACGTTGGAAATCAATGCTTTGGCTAGACAATCG 594
Qy      570  LeuIleAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGlu 589
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Qy      590  MetSerAlaValValTyrLys---AspTyrValPheProGluGlnAlaLeuProThrAsp 608
Db      655  ATGAGTCCGCGGCATACAAAAGCAGCTGCGGTTCGACATGGAAGGCTCCCTGCCGAT 714
Qy      609  LeuIleLysArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeuLeu 628
Db      715  CTAATTCGAGAGAAATGGCAATTCCTGATGCAACACACACCAATGGTCTTAAACTCTCA 774
Qy      629  IleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTyrSerAlaIleLysSerTrp 648
Db      775  ATCGAAGACTATCGTACGCCAACGACGCGTCTTTACTCTGTCGAGCAATCCAAACCTGG 834
Qy      649  ValThrGluTyrCysAsnTyrTyrLysSerAspAlaValGlnLysAspThrGlu 668
Db      835  GTCCGAACCTATGTTGAACGCTACTATCCAAACCCGAACTTATCAAAACAGACTCTGAG 894
Qy      669  LeuGlnAlaTrp---TrpLysGluLeuArgGluGlyHisGlyAspLysLysAspGlu 687
Db      895  CTCCAATGTTGTAGTGGGGGGAATC---AACGTCCGCCACGCTGACCTCCGCGACGCT 951
Qy      688  ProTyrTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIle 707
Db      952  GATTGGTGGCGGAGTTATCAACCGTCGACGACCTCGTGTGATCTTAACCACTCTAATC 1011
Qy      708  TrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyr 727
Db      1012  TGGCTCGCTCTGCTCAACACGCGCTCTAACTTTGGACAATACCCCTTACGTGGGTGCTAC 1071
Qy      728  LeuProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyr 747
Db      1072  GTCCAAACCGCACCGTGTGATCGCGGGTTAATCCCGAGAGTCCGATCCAGAGTAC 1131
Qy      748  GluGluLeuLysThrAsn-ProAspLysValPheLeuLysThrIleThrProGlnLeuG 767
Db      1132  GCGAGTTTCTATCTCCCATCGGAGAGATATTACTTCTCGTCGATGTCGAAGTTTGGCGCA 1191
Qy      767  nThrLeuLeuGlyIleSerLeuIleGluLeuLeuSerArgHisSerSerAspThrLeuTy 787
Db      1192  GACTTCGAAGTTTATGCGCGTGTGATCTTTGTTCGACGCAATTCGCGGATGAGGAGTA 1251
Qy      787  rLeuGlyGlnArgGluSerProGlu---TrpThrLysAspGlnGluProLeuSerAlaph 806
Db      1252  TATTGGAGAGACACACAGCTTCGATTTGGACAGGATCGCGAGATGTTTAAAGCCTT 1311
Qy      806  eAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValas 826

```

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Qy	826	pGlulysTrpLysAsnArgSerClyProvallysValProTyrThrLeuLeuPheProTh	846
Db	1372	TCCTGACCGTAGAAATAGGTGTGGGGCTGGTGTTCGCTTATGAGTTGTGGTTCCGAA	1431
Qy	846	rSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSer	859
Db	1432	GTCGAGCCTGGTGTACGTGTAGAGGTGTACCTAATAGT	1471

Search completed: March 14, 2005, 10:27:33
Job time : 6697 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:39:41 ; Search time 174 Seconds
(without alignments)
1916.020 Million cell updates/sec

Title: US-10-731-642A-1

Perfect score: 4534

Sequence: 1 MFLEKIVDAITKDGKKVK.....LPPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4534	100.0	862	6	Abp70404 Amino aci
2	3695	81.5	857	4	Aab46803 Potato LO
3	3610	79.6	859	6	Abol19443 Wine grap
4	3576	78.9	862	6	Abol19442 Wine grap
5	3022.5	66.7	880	6	AAO27492 Balsam pe
6	2911	64.2	878	4	AAB11500 C. sativu
7	2911	64.2	878	4	AAB86036 Cucumber
8	2905	64.1	857	5	Abg30570 Glycine m
9	2779.5	61.3	864	7	ABW02705 Maize lip
10	2769.5	61.1	864	7	ADG93379 Maize lip
11	2769.5	61.1	864	7	ADG93381 Maize lip
12	2745.5	60.6	865	5	ABG30569 Glycine m
13	2734.5	60.3	887	7	ADG93389 Maize lip
14	2734.5	60.3	887	7	ADG93387 Maize lip
15	2724.5	60.1	887	6	AAO27494 Corn (zea
16	2724.5	60.1	887	7	ADG93393 Maize lip
17	2724.5	60.1	887	7	ADG93391 Maize lip
18	2700.5	59.6	873	7	ADG93371 Maize lip
19	2700.5	59.6	873	7	ADG93373 Maize lip
20	2688	59.3	864	2	AAR24042 Lipoxigen
21	2686.5	59.3	853	2	AAR50220 Soybean l
22	2682	59.2	863	7	ADC53139 9'-specif
23	2680	59.1	862	5	Aau99691 Barley wi
24	2680	59.1	862	5	ABG30566 Wild type
25	2673	59.0	862	5	Aau99693 Barley wi

ALIGNMENTS

RESULT 1

ABP70404
ID ABP70404 standard; protein; 862 AA.

XX AC ABP70404;

XX DT 07-APR-2003 (first entry)

XX DE Amino acid sequence of tobacco lipoxygenase-1 (LOX-1).

KW Lipoxygenase-1; LOX-1; enzyme; plant; dioxygenation;

KW polyunsaturated fatty acid; pentadiene; disease resistance; Solanacea;

KW tobacco; tomato; potato; pepper.

XX OS Nicotiana tabacum.

XX PN WO200299112-A2.

XX PD 12-DEC-2002.

XX PF 06-JUN-2002; 2002WO-FR001943.

XX PR 07-JUN-2001; 2001FR-00007470.

XX PR 07-NOV-2001; 2001FR-00014358.

XX PA (RHOB-) RHOBIO.

XX PI Mene-Safrane L, Esquerre-Tugaye M, Fournier J, Beffa R;

XX PI Grosjean-Cournoyer M;

XX XX WPI; 2003-156858/15.

XX DR N-PSDB; ABZ68210.

XX PT Reducing sensitivity of plants to diseases and pathogens, by overexpressing a lipoxygenase, also vectors and cassettes for the process and transformed plants.

XX PS Claim 7; Page 39-41; 47pp; French.

XX CC The present sequence represents a lipoxygenase-1 (LOX-1) gene. LOX-1 is an enzyme that catalyses the dioxygenation of polyunsaturated fatty acids having a pentadiene system. Overexpression of LOX-1 can be used to reduce the sensitivity of plants to diseases and attack by pathogens.

XX CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi and insects, in a wide range of crops, particularly the Solanaceae, e.g. tobacco, tomato, potato and pepper

XX SQ Sequence 862 AA;

26	2673	59.0	862	5	Aau99692 Barley wi
27	2673	59.0	862	5	Abg30567 Mutant ty
28	2672.5	58.9	837	6	Ada48504 Rice prot
29	2656	58.6	839	5	Abg30568 Glycine m
30	2585.5	57.0	871	7	Adg93383 Maize lip
31	2585.5	57.0	871	7	Adg93385 Maize lip
32	2584.5	57.0	864	5	Abg30571 Barley lo
33	2563	56.5	865	2	Aar23797 Rice lipo
34	2563	56.5	865	2	Aar20670 Lipoxygen
35	2096.5	46.2	842	7	Adg93421 Maize lip
36	2096.5	46.2	842	7	Adg93419 Maize lip
37	1934	42.7	919	8	Adn72259 Thale cre
38	1906.5	42.0	491	7	Aae39891 Human lip
39	1906.5	42.0	491	8	Adg48421 Lipoxygen
40	1843.5	40.7	892	7	Adg93395 Maize lip
41	1843.5	40.7	892	7	Adg93397 Maize lip
42	1840.5	40.6	807	7	Adg93413 Maize lip
43	1840.5	40.6	807	7	Adg93411 Maize lip
44	1814	40.0	896	8	Adn73207 Thale cre
45	1788	39.4	924	6	Aae38266 Rice dise

Query Match	100.0%;	Score 4534;	DB 6;	Length 862;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 862;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFLEKIVDAITGDKGKVKGTIVLMKKNVLDFTDINASVLDGVLGFLGRRVSLLEISV	60	
Db	1	MFLEKIVDAITGDKGKVKGTIVLMKKNVLDFTDINASVLDGVLGFLGRRVSLLEISV	60	
QY	61	NADPANGLOGKRSKAAYLENLWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFS	120	
Db	61	NADPANGLOGKRSKAAYLENLWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFS	120	
QY	121	EFFLSLTLEVPNHGKHVHCNSWVYPANKYKSDRIFFANQAYLPSETDPTLRKYRENE	180	
Db	121	EFFLSLTLEVPNHGKHVHCNSWVYPANKYKSDRIFFANQAYLPSETDPTLRKYRENE	180	
QY	181	LVTLRGDTGKLEEDRWYVYAYNDLGDPPKQDLSRPVLGGSSEYPPRRGRTGRKPT	240	
Db	181	LVTLRGDTGKLEEDRWYVYAYNDLGDPPKQDLSRPVLGGSSEYPPRRGRTGRKPT	240	
QY	241	KTDPNSESRIPLMSLDIYVPRDERFGHIKLSDFLTFALKSIIVQLLLPEFKALFDSHTNE	300	
Db	241	KTDPNSESRIPLMSLDIYVPRDERFGHIKLSDFLTFALKSIIVQLLLPEFKALFDSHTNE	300	
QY	301	FDSFEDVLKYEKGKIKLQGPLLKAITDSIPLEILKELLRSNDEGLFKYPTPQVIOEDKT	360	
Db	301	FDSFEDVLKYEKGKIKLQGPLLKAITDSIPLEILKELLRSNDEGLFKYPTPQVIOEDKT	360	
QY	361	AWRTDEEFGREMLAGVNPVVISRLQEPFKSKLDPKIYGNQNSTITRQIEDKLDGLTID	420	
Db	361	AWRTDEEFGREMLAGVNPVVISRLQEPFKSKLDPKIYGNQNSTITRQIEDKLDGLTID	420	
QY	421	EAIKTNRLFILNHHIDILMPYLRINTSDTKTYASRTLLFTQDNQTLKPSAIELSLPHD	480	
Db	421	EAIKTNRLFILNHHIDILMPYLRINTSDTKTYASRTLLFTQDNQTLKPSAIELSLPHD	480	
QY	481	GDQFAGVSKVYTPADQGVGSIWOLAKAYAVNDGSGVHQLISHLNTHAAIEPFVIATNR	540	
Db	481	GDQFAGVSKVYTPADQGVGSIWOLAKAYAVNDGSGVHQLISHLNTHAAIEPFVIATNR	540	
QY	541	QLSALHPIYKLLHPIHFRMTNINALARQILINGGGLLELTVPFPAKYSMEGSAVYKDWVF	600	
Db	541	QLSALHPIYKLLHPIHFRMTNINALARQILINGGGLLELTVPFPAKYSMEGSAVYKDWVF	600	
QY	601	PRQALPTDLIKRGVAVEDSSPLGIRLLIQQYPAVDGLKIWSAITSKSWTEYCNYIYKSD	660	
Db	601	PRQALPTDLIKRGVAVEDSSPLGIRLLIQQYPAVDGLKIWSAITSKSWTEYCNYIYKSD	660	
QY	661	DAVQKDTLQAWKELREEGHGDKDEPWPQKQVQVQELIDSCITTIWIASALHAANFG	720	
Db	661	DAVQKDTLQAWKELREEGHGDKDEPWPQKQVQVQELIDSCITTIWIASALHAANFG	720	
QY	721	QYPYAGYLPNRPRTLGRNFMPEPGSPYBELKTNPKVFLKTTIPQQLIGLSLIEILSR	780	
Db	721	QYPYAGYLPNRPRTLGRNFMPEPGSPYBELKTNPKVFLKTTIPQQLIGLSLIEILSR	780	
QY	781	HSSDTLYLQGRESPTWKQEPISAFARPGKLSIDEDQIMQNVDEKWNKNSGPKVPY	840	
Db	781	HSSDTLYLQGRESPTWKQEPISAFARPGKLSIDEDQIMQNVDEKWNKNSGPKVPY	840	
QY	841	TLLFPTSEGLTGKIPNSVSI	862	
Db	841	TLLFPTSEGLTGKIPNSVSI	862	

RESULT 2

AAB46803

ID AAB46803 standard; protein; 857 AA.

XX

AC AAB46803;

XX

DT 23-APR-2001 (first entry)

XX	Potato LOX protein.	
DE		
XX	Potato; LOX protein; lipoxygenase; arachidonic acid; mutant; plant;	
KW	11-arachidonate-lipoxygenase; 11-hydroperoxy-arachidonic acid.	
XX		
OS	Solanum tuberosum.	
FN	W0200104323-A2.	
XX		
PD	18-JAN-2001.	
XX		
PF	10-JUL-2000; 2000WO-EP006539.	
XX		
PR	08-JUL-1999; 99DE-01031819.	
XX		
PA	(IPBP-) IPB INST PFLANZENBIOCHEMIE.	
XX		
PI	Feussner I, Hornung E, Rosahl S;	
XX		
DR	WPI; 2001-081054/09.	
XX		
PT	New nucleic acid encoding lipoxygenase useful for producing 11-	
PT	hydroperoxy- or hydroxy-arachidonic acid.	
XX		
PS	Disclosure; Fig 3; 18pp; German.	
XX		
CC	This invention describes a novel nucleic acid (I) encoding a potato	
CC	lipoxygenase protein, LOX, (II) is new. The invention also describes (1)	
CC	(II), a sequence of 857 amino acids (aa), given in the specification; (2)	
CC	a vector (III) comprising (I); (3) a host cell (IV) comprising (I) or	
CC	(III); (4) a plant or part of a plant comprising (IV); (5) enhancing the	
CC	specificity of a plant lipoxygenase for position 11 of arachidonic acid	
CC	comprises mutating at least one amino acid of the wild type lipoxygenase;	
CC	(6) producing 11-hydroperoxy-arachidonic acid or the reduced 11-hydroxy-	
CC	derivative comprises treating arachidonic acid with (II) and further	
CC	reducing the obtained hydroperoxy form to the hydroxy form; (7) the	
CC	arachidonic acid derivative, comprising a hydroperoxy group or a hydroxy	
CC	group at position 11. (II) is useful for producing 11-hydroperoxy-	
CC	and/or 11-hydroxy-arachidonic acid. The lipoxygenase is specific for	
CC	position 11 of arachidonic acid	
XX	Sequence 857 AA;	
SQ		
Query Match 81.5%; Score 3695; DB 4; Length 857;		
Best Local Similarity 80.0%; Pred. No. 6.4e-310;		
Matches 682; Conservative 84; Mismatches 85; Indels 2; Gaps 2;		
QY	10	ITGDDGKKVGTIVLMKKNVLDFTDINASVLDGVLGFLGRRVSLLEISVSNADPANGLQ 69
Db	7	IGGHHDSKKVGTIVLMKKNVLDFTDINASVLDGVLGFLGRRVSLLEISVSNADPANGLQ 66
QY	70	GKRKAAYLENLWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHSEFFLKSITL 129
Db	67	GKSNPAYLENLWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHSEFFLKSITL 125
QY	130	EDVNHGKHVHCNSWVYPANKYKSDRIFFANQAYLPSETDPTLRKYRENEELTLRGDGT 189
Db	126	EDVNHGKHVHCNSWVYPANKYKSDRIFFANQAYLPSETDPTLRKYRENEELTLRGDGT 185
QY	190	GKLEBWDRVYAYNDLGDPPKQDLSRPVLGGSSEYPPRRGRTGRKPTKTDPNSSSR 249
Db	186	GKLEBWDRVYAYNDLGDPPKQDLSRPVLGGSSEYPPRRGRTGRKPTKTDPNSSSR 245
QY	250	IPLMSLDIYVPRDERFGHIKLSDFLTFALKSIIVQLLLPEFKALFDSHTNEFDSFEDVLK 309
Db	246	IPLMSLDIYVPRDERFGHIKLSDFLTFALKSIIVQLLLPEFKALFDSHTNEFDSFEDVLK 305
QY	310	LYEGGIKLPQGLPFLKALTAALPLEMKELLTDEGILRFTPLVIKDKSKTAWRTDEBFG 369
Db	306	LYEGGIKLPQGLPFLKALTAALPLEMKELLTDEGILRFTPLVIKDKSKTAWRTDEBFG 365
QY	370	REMLAGVNPVVISRLQEPFKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLF 429

Db 600 QALPADLIRKRGMAVEDSEAPHGRLRLIDDYPVAVDGLSIAETWVKEYCSFYKTD 659
Qy 663 VOKOTELQAWKELREBEGDKKDPWPKMOTVOELIDSCITITIIWASALHAANFQY 722
Db 660 VOKDSELOSWKKEVREBEGDKKDPWPKMOTVKELIETCTIIWASALHAANFQY 719
Qy 723 PVAGVLPNRPPTLSRPFMPGSPPEVEELKTNPKVFLKTIITPOLQTLGSLIETLSRHS 782
Db 720 PVAGVLPNRPPTLSRPFMPGSPPEVEELKSNPKAFKTIITAOQLTLGSLIETLSRHS 779
Qy 783 SDTLYLGQRESPEWTKDQEPISAFARFGKGLSDIEDQIMQNVDEKKNRSPVKVPYTL 842
Db 780 SDEVVLGQDTPFWLDTITPLKAFKFGKGLADIEIMIDRNGNERFKNRGPVKIPYTL 839
Qy 843 LPPTSEGGITGKIPNSVSI 862
Db 840 LYPTSEGGITGKIPNSVSI 859

RESULT 4
ID ABO19442
XX ABO19442 standard; protein; 862 AA.
AC ABO19442;
XX AC
DT 27-AUG-2003 (first entry)
XX
DE Wine grape lipoxigenase LOX1.
XX
KW Wine grape; lipoxigenase; LOX; flavour; fermented beverage; enzyme;
KW grape juice; cheese; yogurt; pickle; tissue specificity; timing; wine.
XX
OS Vitis vinifera.
XX
PN US2003033627-A1.
XX
PD 13-FEB-2003.
XX
PF 16-OCT-2001; 2001US-00978522.
XX
PR 16-OCT-2000; 2000US-0241220P.
XX
PA (DESC/) DESCENZO R A.
PA (IREL/) IRELAN N A.
XX
PI Descenzo RA, Irelan NA;
XX
DR WPI; 2003-492095/46.
DR N-PSDB; AC028851.
XX
PT Novel purified and isolated Vitis vinifera lipoxigenase polypeptide,
PT useful for modifying the flavor of a comestible e.g., a beverage which is
PT a fermentation product, preferably wine.
XX
PS Claim 7; Page 14; 36pp; English.
XX
CC The invention relates to a purified and isolated Vitis vinifera
CC lipoxigenase (LOX) polypeptide. The polypeptide is useful for modifying
CC the flavour of a comestible e.g. a beverage which is a fermentation
CC product, preferably wine. The polypeptide is useful for analysing the
CC effect of LOX polypeptides on flavour production in wine and grape juice.
CC The polypeptide is useful in the production of cheese, yogurt, pickles
CC etc. The polypeptide is also useful in screening assays to identify
CC modulators that modulate the activity of the Vitis vinifera LOX
CC polypeptides. The polynucleotide is useful in heterologous production of
CC pure lipoxigenase enzyme in a protein expression vector and for studying
CC the native level of gene expression in response to environmental or
CC viticultural influences. The cloned gene can be used to produce
CC transgenic plants to modify the level of gene expression to produce
CC optimal levels of lipoxigenase in the grape. Knowledge of Vitis vinifera
CC lipoxigenase coding DNA sequences allows for modification of cells to
CC permit, increase or decrease, expression of endogenous Vitis vinifera

CC lipoxigenase. Such knowledge also permits modification of timing and
CC tissue specificity of LOX expression. The DNA sequence information also
CC makes possible the development through, e.g. homologous recombination or
CC knock-out strategies of grapes that fail to express functional
CC lipoxigenase or that express a variant of Vitis vinifera lipoxigenase.
CC Such plants are useful as models for studying the in vivo activities of
CC Vitis vinifera lipoxigenase and modulators of Vitis vinifera
CC lipoxigenase. The present sequence represents the amino acid sequence of
CC a wine grape lipoxigenase LOX
XX
SQ Sequence 862 AA;
Query Match 78.9%; Score 3576; DB 6; Length 862;
Best Local Similarity 76.2%; Pred. No. 1.3e-299;
Matches 655; Conservative 109; Mismatches 94; Indels 2; Gaps 2;
Qy 3 LEKIVDAITGKDDKKVKGTVLWKNVLDPTDINASVLDGVLEFLGRVRSLELISSVNA 62
Db 5 LLSIVSAITGENDKKIEGTIVLWKNVLDPTDINAPVRDRVHLEFGQVSLVSAVHG 64
Qy 63 DPANGLOGKRKAAYLENWLTNSTPIAAGESAFRTVTDWDEEGVPCAFIINKLHSEF 122
Db 65 DPANGLOGKRGKPAYLEDWITITSLTAGESAFKVTFDW-DEEIGPCAFIRNNHSEF 123
Qy 123 FLKSITLEDVFNHGKVFHVCNSWYYPANKYKSDRIFFANQAYLPSETDTLTKYRENELV 182
Db 124 YLRITLEDVFNHGKVFHVCNSWYYPANKYKSDRIFFANQAYLPSETDTLTKYRENELV 183
Qy 183 TLRGDTGKLEWRVYDYAYNDLGDPPKQDLSRPVLGSSSEYYPARGTGRPKPT 242
Db 184 NLRGDTGKLEWRVYDYAYNDLGDPPKQDLSRPVLGSSSEYYPARGTGRPKPT 243
Qy 243 DPNSERPLWMSLDIYVPRDERFGHKLSDPLFALKSIIVQLLLPEFKALFDSFHNFD 302
Db 244 DPKTESRPLWMSLDIYVPRDERFGHKLSDPLFALKSIIVQLLLPEFKALFDSFHNFD 303
Qy 303 SFEDVLKLYEGGIKLPQGPLLKAITDSIPLLEIKELRSDEGLPKYPTPQVIOEDKTAW 362
Db 304 SFQDVLDIYEGGIKVPGEPLDKIKDNIPLKELVTDGEHLFKFPMPOVVKEDKSAW 363
Qy 363 RTDEFGREMLAGVNPVILSRLOFPKPKSLDPKIYGNQNSTITREQIEDKLDGTLIDEA 422
Db 364 RTDEFGREMLAGVNPVILSRLOFPKPKSLDPKIYGNQNSTITREQIEDKLDGTLIDEA 423
Qy 423 IKTNRLFLNHHDIILPVLRRINTSTDTKTASRTLLFLQDNGTLKPSAIELSLPHDGD 482
Db 424 MEKRLFLNHHDIILPVLRRINTSTDTKTASRTLLFLQDNGTLKPSAIELSLPHDGD 482
Qy 483 QFGAVSKVYTPADQVEGSIWQAKAYAAVNDSGVHQLISHWLNTHAAIEPFIATNRQL 542
Db 483 KFGAVSKVYTPADQVEGSIWQAKAYAAVNDSGVHQLISHWLNTHAAIEPFIATNRQL 542
Qy 543 SALHPIYKLLHPHRETWNINARQIILINGGGLLELTVFPKAYKMSMVAVYKDWVPE 602
Db 543 SVLHPHKLHPHRETWNINARQIILINGGGLLELTVFPKAYKMSMVAVYKDWVPE 602
Qy 603 QALPTDLIKRGVAVEDSSPLGIRLLIODYPVAVDGLKWSAISKWTEYCNYYKSDA 662
Db 603 QALPADLIRKRGMAVEDSEAPHGRLRLIDDYPVAVDGLSIAETWVKEYCSFYKTD 662
Qy 663 VOKOTELQAWKELREBEGDKKDPWPKMOTVOELIDSCITITIIWASALHAANFQY 722
Db 663 VOKDSELOSWKKEVREBEGDKKDPWPKMOTVKELIETCTIIWASALHAANFQY 722
Qy 723 PVAGVLPNRPPTLSRPFMPGSPPEVEELKTNPKVFLKTIITPOLQTLGSLIETLSRHS 782
Db 723 PVAGVLPNRPPTLSRPFMPGSPPEVEELKSNPKAFKTIITAOQLTLGSLIETLSRHS 782
Qy 783 SDTLYLGQRESPEWTKDQEPISAFARFGKGLSDIEDQIMQNVDEKKNRSPVKVPYTL 842
Db 783 SDEVVLGQDTPFWLDTITPLKAFKFGKGLADIEIMIDRNGNERFKNRGPVKIPYTL 842
Qy 843 LPPTSEGGITGKIPNSVSI 862

843 LYPTSEGLTGKIPNSVSI 862

Db

AAO27492

AAO27492 standard; protein; 880 AA.

XX

AAO27492;

XX

06-NOV-2003 (first entry)

XX

Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.

XX

Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;

KW

fatty acid metabolite synthesis; signal molecule; growth regulation;

KW

development regulation; plant development; wound response;

KW

genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.

XX

Momordica charantia.

OS

US2003074693-A1.

PN

17-APR-2003.

PD

29-JAN-2002; 2002US-00059909.

PF

10-FEB-1999; 99US-0119597P.

PR

09-FEB-2000; 2000US-00501422.

XX

(CAHO) CAHOON E B.

PA

(KIN) KINNEY A J.

PA

(KLEI) KLEIN T M.

PA

(LEEJ) LEE J.

PA

(PEAR) PEARLSTEIN R W.

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(RAFA) RAFALSKI J A.

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(SHEN) SHEN J B.

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(THOR) THORPE C J.

PA

(TING) TINGEY S V.

PA

(WENG) WENG Z.

XX

Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;

PI

Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;

XX

WPI; 2003-567325/53.

DR

N-PSDB; AAL57712.

XX

New isolated polynucleotides encoding plant lipoxigenases, useful in

PT

genetic mapping, particularly in catalyzing hyperoxidation of

PT

polyunsaturated fatty acids.

XX

Claim 19; Page 23-25; 36pp; English.

XX

This invention relates to novel nucleotide sequences which encode

CC

proteins which have lipoxigenase activity. Lipoxigenases are membrane

CC

bound ubiquitous enzymes which catalyse the hydroperoxidation of

CC

polyunsaturated fatty acids in the first step of fatty acid metabolite

CC

synthesis. Products of this pathway are found as signal molecules

CC

involved in growth and development regulation. A knowledge of the amino

CC

acid sequence of lipoxigenases may allow the understanding of plant

CC

development and wound response. The polynucleotides, polypeptides and

CC

lipoxigenases of the invention may therefore be useful in genetic mapping

CC

and particularly for catalysing hydroperoxidation of polyunsaturated

CC

fatty acids. The present sequence is the amino acid sequence of the

CC

Balsam pear (Momordica charantia) lipoxigenase protein 2 of the invention

XX

Sequence 880 AA;

SQ

Query Match

Best Local Similarity

Matches 554; Conservative 132; Mismatches 156; Indels 5; Gaps 4;

16 GKKVGTVVLAKKNVLDFTDINASVLDGVLEPLGRVRSLELITSSVSNADPANGLOGKRSKA 75

Query

843 LYPTSEGLTGKIPNSVSI 862

AAO27492

AAO27492 standard; protein; 880 AA.

AAO27492;

06-NOV-2003 (first entry)

Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.

Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;

fatty acid metabolite synthesis; signal molecule; growth regulation;

development regulation; plant development; wound response;

genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.

Momordica charantia.

US2003074693-A1.

17-APR-2003.

29-JAN-2002; 2002US-00059909.

10-FEB-1999; 99US-0119597P.

09-FEB-2000; 2000US-00501422.

(CAHO) CAHOON E B.

(KIN) KINNEY A J.

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(WENG) WENG Z.

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WPI; 2003-567325/53.

N-PSDB; AAL57712.

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involved in growth and development regulation. A knowledge of the amino

acid sequence of lipoxigenases may allow the understanding of plant

development and wound response. The polynucleotides, polypeptides and

lipoxigenases of the invention may therefore be useful in genetic mapping

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fatty acids. The present sequence is the amino acid sequence of the

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Sequence 880 AA;

Query Match

Best Local Similarity

Matches 554; Conservative 132; Mismatches 156; Indels 5; Gaps 4;

16 GKKVGTVVLAKKNVLDFTDINASVLDGVLEPLGRVRSLELITSSVSNADPANGLOGKRSKA 75

Query

843 LYPTSEGLTGKIPNSVSI 862

AAO27492

AAO27492 standard; protein; 880 AA.

AAO27492;

06-NOV-2003 (first entry)

Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.

Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;

fatty acid metabolite synthesis; signal molecule; growth regulation;

development regulation; plant development; wound response;

genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.

Momordica charantia.

US2003074693-A1.

17-APR-2003.

29-JAN-2002; 2002US-00059909.

10-FEB-1999; 99US-0119597P.

09-FEB-2000; 2000US-00501422.

(CAHO) CAHOON E B.

(KIN) KINNEY A J.

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(WENG) WENG Z.

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WPI; 2003-567325/53.

N-PSDB; AAL57712.

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This invention relates to novel nucleotide sequences which encode

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Sequence 880 AA;

Query Match

Best Local Similarity

Matches 554; Conservative 132; Mismatches 156; Indels 5; Gaps 4;

16 GKKVGTVVLAKKNVLDFTDINASVLDGVLEPLGRVRSLELITSSVSNADPANGLOGKRSKA 75

Query

843 LYPTSEGLTGKIPNSVSI 862

AAO27492

AAO27492 standard; protein; 880 AA.

AAO27492;

06-NOV-2003 (first entry)

Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.

Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;

fatty acid metabolite synthesis; signal molecule; growth regulation;

development regulation; plant development; wound response;

genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.

Momordica charantia.

US2003074693-A1.

17-APR-2003.

29-JAN-2002; 2002US-00059909.

10-FEB-1999; 99US-0119597P.

09-FEB-2000; 2000US-00501422.

(CAHO) CAHOON E B.

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(TING) TINGEY S V.

(WENG) WENG Z.

Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;

Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;

WPI; 2003-567325/53.

N-PSDB; AAL57712.

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synthesis. Products of this pathway are found as signal molecules

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Query Match

Best Local Similarity

Matches 554; Conservative 132; Mismatches 156; Indels 5; Gaps 4;

16 GKKVGTVVLAKKNVLDFTDINASVLDGVLEPLGRVRSLELITSSVSNADPANGLOGKRSKA 75

Query

843 LYPTSEGLTGKIPNSVSI 862

AAO27492

AAO27492 standard; protein; 880 AA.

AAO27492;

06-NOV-2003 (first entry)

Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.

Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;

fatty acid metabolite synthesis; signal molecule; growth regulation;

development regulation; plant development; wound response;

genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.

Momordica charantia.

US2003074693-A1.

17-APR-2003.

29-JAN-2002; 2002US-00059909.

10-FEB-1999; 99US-0119597P.

09-FEB-2000; 2000US-00501422.

(CAHO) CAHOON E B.

(KIN) KINNEY A J.

(KLEI) KLEIN T M.

(LEEJ) LEE J.

(PEAR) PEARLSTEIN R W.

(RAFA) RAFALSKI J A.

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(THOR) THORPE C J.

(TING) TINGEY S V.

(WENG) WENG Z.

Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;

Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;

WPI; 2003-567325/53.

N-PSDB; AAL57712.

New isolated polynucleotides encoding plant lipoxigenases, useful in

genetic mapping, particularly in catalyzing hyperoxidation of

polyunsaturated fatty acids.

Query Match	64.2%;	Score 2911;	DB 4;	Length 878;
Best Local Similarity	62.3%;	Pred. No. 4.8e-242;		
Matches 534;	Conservative 140;	Mismatches 175;	Indels 8;	Gaps 6;
QY	6	IVDAITGDDGKKVGTGVVLMKKVLDFTDINASVLDGVLEFLGRRVSLLEISSVNADPA	65	
Db	30	ILDRVSSL-GGNKIRGVLMRSNVLDFTEPHSNLLDNFTLLGGVSPQLISATHT--S	86	
QY	66	NCLQGRSKAAYLENLNSTPIAGESAFTVTFDWDDEFGVPGCAFIKNLHFSEFLK	125	
Db	87	NDSRGKGVGNKAYLEWLTSIPPLFAGESVFQINFQW-DENFGPGAFPTKNGHTSEFLK	145	
QY	126	SLTLEDVPHNGHVHFCNSWVYPANKYKSDRIFFANQAYLPSETDTRLKRYRENEILVTLR	185	
Db	146	SLTLDVVCYGRVHFDCHSWVPSGRYKQDRIFFANVHVLPSQTPNPLKRYRENEILVTLR	205	
QY	186	GDGTGKLEEDRVYDYYNDIGDPKQDLSRPVGLSGSEYPPRRGRTGRKPTKTDPN	245	
Db	206	GDGTGERKEDRIYDVYNDIADPDVGD--HRPILGGTTEYPPRRGRTGRPRSRDHN	263	
QY	246	SESRIPLMSLDIYVPRDRFGHKLSDPLTALAKSIYQLLLPEPKALFDSTHNEFDSPE	305	
Db	264	YESRLSPIMSLDIYVPRDGFHKLKSDPLGLYTLKALSISIKPGLQSLFDVTPNEFDNFK	323	
QY	306	DVLKLYEGGKLPQGPFLKAITDSIPLEILKELRSDBGELFKYPTPOVIOEDKTAWRTD	365	
Db	324	EVDNLFERGFPIFPN-AFKLTLEDITPPLFKALVRNDGEKFKFTPEVVKDNKLGWSTD	382	
QY	366	EEFGREMLAGVNPVIAISRLQEPKPSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAINT	425	
Db	383	EEFAREMLAGVNPVLIIRLEAFPPTSKLDPNVYGNQNSTITEEIKHGLDGLTIDEAMKQ	442	
QY	426	NRLFTLNHHDILMPYLRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHPGDQFG	485	
Db	443	NRLYIVDFHDALMPYLRMN-ATSTKTYATRTLLKDDGTLLKPLVIELALPHPGDQDILG	501	
QY	486	AVSKYVTPADQGVESIWOLAKAYAVNDGSHVQLISHWLNTHAAIEPPVIATNRQLSAL	545	
Db	502	AISKUYFFAENGQVKSINOLAKAYVTVNDGVHQLISHWLNTHAAIEPPVIATNRQLSAL	561	
QY	546	HPYKLLHPHRETNNALARQILINGGLLELTVPFAKYSMEMSAVVYKDWVPPEQAL	605	
Db	562	HPHKLAVPHYKDTWFINASARQVLINANGLIETTHYPSKYSMELSSILYKDWTFDQAL	621	
QY	606	PTDLIKRGVAVEDSSPGLIRLLIODYPAVDGLKIWSAIKSWTEYCNYYKSDDAVQK	665	
Db	622	PNNLMKRLAVEDSSAPHGRLRLINDYPPAVDGLDIWSAIKTWQDYCCLYYKDDNAVQN	681	
QY	666	DTELQAWKELREEGHGDKDEPMPKQVOTVDELIDSCITTIWIASALHAAVNFQYPA	725	
Db	682	DFELQSWNELREKHAQKHEPWPQKQVOTSELIESCTTIWIASALHAAVNFQYPA	741	
QY	726	GYPNRPRLSRNFMPEPGSPSEELKTNPKDFLKTITPQLOTLGLISLIETLSRHSST	785	
Db	742	GYPNRPRLSRNFMPEPGSPSEELKTNPKDFLKTITPQLOTLGLISLIETLSRHSST	801	
QY	786	LYLGQRESEPTKQDEPISAFARFGKULSDIEDQIMQMVNDKKNRSGPVKVPYTLTLP	845	
Db	802	VYLGQASIDWTSRDKIALEAFKFGKULFEVENIRMERKNVKNRSGPVNLPYTLTLP	861	
QY	846	TSEGLTGKGPNSVSI	862	
Db	862	SSNEGLTGKGPNSVSI	878	
RESULT 8				
ABG30570				
ID	ABG30570	standard; protein; 857 AA.		
XX				
AC	ABG30570;			
XX				
DT	07-OCT-2002	(first entry)		

XX	Glycine max low-lipoxygenase 3 (LOX-3).
DE	Lipoxygenase-1; LOX-1; beverage; malt; beer; organoleptic property;
XX	brewing; trans-2-nonenal; flavour stability; storage; shelf-life;
KW	low-lipoxygenase 3.
KW	Glycine max.
OS	WO200253721-A1.
XX	11-JUL-2002.
XX	22-JAN-2001; 2001WO-IB000207.
XX	29-DEC-2000; 2000US-00751687.
PR	29-DEC-2000; 2000WO-IB002045.
XX	(CARL-) CARLSBERG RES LAB.
PA	(HETB) HEINEKEN TECH SERVICES BV.
PA	(BRAS-) BRASSERIES KRONENBOURG SA.
XX	Douma AC, Dodéer A, Cameron-Mills V, Skadhauge B, Bech LM;
PI	Schmitt N, Heistek JC, Van Mechelen JR;
PI	WPI; 2002-557742/59.
XX	Novel barley plants having low lipoxygenase activity useful in the
PT	production of plant products such as malt or brewed beverages,
PT	particularly beer having increased stability and flavor.
XX	Disclosure; Fig 22A-B; 112pp; English.
PS	The invention describes a barley plant (I) having a mutant lipoxygenase-1
XX	(LOX-1) protein, the plant or plant portion characterised by a reduction
CC	or absence of LOX activity as compared to a non-mutated control, or
CC	comprising a heterologous nucleic acid sequence expressing an antisense
CC	sequence to a transcribed region of barley lpx-1 gene, operably linked to
CC	a promoter and a transcription terminator sequence (II), a plant (III)
CC	produced using (I) or a plant product (III) is useful in the manufacture
CC	of a beverage, preferably malt or beer, for stabilising organoleptic
CC	properties of a brewed product over a measured period of time as compared
CC	to a control brewed product produced using a non-mutated barley plant or
CC	its portion, grain or plant progeny, or plant product, and for the
CC	manufacture of a brewed product having reduced levels of free trans-2-
CC	nonenal over a measured period of time or under conditions of elevated
CC	storage temperature, as compared to a control brewed product produced
CC	using a non-mutated barley plant or its portion, grain or plant product.
CC	Beer with significantly enhanced flavour stability, both during storage
CC	and on exposure to elevated storage temperatures is obtained. These
CC	properties enhance the quality of beer and are useful to extend its shelf
CC	-life and reduce the need to cool beer during transport and storage. This
CC	is the amino acid sequence of the Glycine max low-lipoxygenase 3 (lox-3)
CC	protein
XX	Sequence 857 AA;
SQ	Query Match 64.1%; Score 2905; DB 5; Length 857;
	Best Local Similarity 63.3%; Pred. No. 1.5e-241;
	Matches 548; Conservative 122; Mismatches 160; Indels 36; Gaps 9;
QY	16 GKVKGTVLMKKVLDFT-----DINASVLDGVLEFLGRRVSLLEISSVNA 62
Db	9 GHKRGTVLMKRNKVLDSVTSVGGIIGQGLLDVGVSTLDTLTAFLGRSVSLQLSATKA 68
QY	63 DPANGLOGRSKAAYLENLNSTPIAGESAFTVTFDWDDEFGVPGCAFIKNLHFSEF 122
Db	69 D-ANG-KCKLGAFTLEGIITSLPTLGAGSAFKINFEDDGS-GIPGAFYIKNFMQTEF 125
QY	123 FLKSLTLEDVPHNGHVHFCNSWVYPANKYKSDRIFFANQAYLPSETDTRLKRYRENEILV 182
Db	126 FLVSLTLEDIPNHGSIHFCVNCNWIYNAKLKFSKDRIFFFANQAYLPSETDTRLKRYRENEILV 185

183 TLRGDGTGKLEWDRVYAYVNDLGDGDKDLSRPVGLGSSEYVPRRGRTRGKPTKT 242
 186 NLRGDTGGERKEWERYDYDVNDLGDGDKENHARPVLGNDTFPPRRGRTRGKPTRK 245
 243 DPNSERIPILMSLDIYVPRDERFGHKLSDFLTPALKSIYQLLPEPKALFD--STHNE 300
 246 DPNSER-----SNDVPLPRDEAFGLKSSDFTLVGLKSVQNVPLPLQSAFDLNFTR 300
 301 FDSFEDVLKVEGGIKLPGQLLKAITDSI-----PLEILKELLSDDGGLFKYPTPQVIO 356
 301 FDSFEDVGLYSGGKLP-----TDIISKISPLPVKEIFRDTGEQALKFPPPKVIO 352
 357 EDKTAWRDDEFGREMLAGVNPVIISRLQEPPEPKSLDPKLYGNQNSTITREQIEDKLDG 416
 353 VSKSAWMTDEEFARMLAGVNPVIRLCKDPPRSKLSQVGDHTSQITKEHLEPNLEG 412
 417 LTIDEAIKTRNLFILNHRDILMPYLIRINTSDTKTYASRTLLFLQDNGTLKPSAIELSL 476
 413 LTVDEAIQNKRLFLDHDHPIMPYLRRIN-ATSTKAYATRIFLKNDGTLRPLAIELSL 471
 477 PHPDGQFGAVSKVYTPADQGVESIWQAKAYAAVNDSGVHQLISHWLNTHAAIEPVI 536
 472 PHPDGQSGAFSQVLPADQGVESIWLLAKAYVYVNDSCYHQLVSHWLNTHAVVEPFI 531
 537 ATNROLSALHPYKLLHPRFETMINALARQILINGGLLELTVFPKYSMEASVYVK 596
 532 ATNRLHSVVHPYKLLHPRFETMINALARQILINGGLLELTVFPKYSMEASVYVK 591
 597 DWVFPQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKWTEYCNYY 656
 592 DWVFTDQALPADLIRKGAIEDSPCHGIRLVIEDYPTVDGLEIWDKATWVHEVFLY 651
 657 YKSDDAVOKDTLOAWKELBEHGDGKDEFPWPKMOTVQELIDSCTITWIASALHAA 716
 652 YKSDTLREDEPQACWELVEVGHGDKNEPWPKNQTRTELVEACAIITWIASALHAA 711
 717 VNFQGPYVAGYLPNRPITLSRNPMPGSPYEELKTNPKVFLKTTITPOLOTLLGISLIE 776
 712 VNFQGPYVGGILNRPITLSRNPMPGSAEYELKRNPKQAYLKITPKFQTLIDLVSIE 771
 777 ILSRHSSTLYLGQRESPEWTKDQBPPLSAFARFGKLSIDIEDQIMQNVDEKMRSGPV 836
 772 ILSRHSDEVYLGERNPNWTSRTRALEAFKFGNKLQAIENKLSERNDEKLRNRCGPV 831
 837 KVPYTLPTSEGGITGKIPNSVSI 862
 832 QMPYTLTLLPSKEGLTRGIPNSISI 857

RESULT 9
 ABW02705
 ID ABW02705 standard; protein; 864 AA.
 AC ABW02705;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Maize lipoxigenase (CSSAP92) protein.
 XX
 KW Maize; lipoxigenase; CSSAP92; aflatoxin; gene therapy; plant protectant;
 KW enzyme.
 XX
 OS Zea mays.
 XX
 PN US6627797-B1.
 XX
 PD 30-SEP-2003.
 XX
 PF 16-MAR-2001; 2001US-00810268.
 XX
 PR 21-MAR-2000; 2000US-0190950P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.

PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Duwick J, Maddox JR, Keller NP;
 XX
 DR WPI; 2003-874315/81.
 DR N-PSDB; AAD64728.
 XX
 PT New maize lipoxigenase polynucleotide, designated CSSAP92, useful for
 PT altering lipoxigenase concentration in plants, for decreasing
 PT accumulation of aflatoxin in plants, or for increasing the resistance of
 PT plants to pathogens.
 XX
 PS Claim 1; SEQ ID NO 3; Opp; English.
 XX
 CC The invention relates to maize lipoxigenase polynucleotide, designated
 CC CSSAP92. The nucleic acid molecule and methods are useful in altering
 CC lipoxigenase concentration in plants, in decreasing accumulation of
 CC aflatoxin in plants, or in increasing the resistance of plants to
 CC pathogens. The invention is useful in gene therapy. The present sequence
 CC is the maize lipoxigenase protein
 XX
 SQ Sequence 864 AA;
 Query Match 61.3%; Score 2779.5; DB 7; Length 864;
 Best Local Similarity 60.6%; Pred. No. 1.1e-230;
 Matches 525; Conservative 124; Mismatches 207; Indels 11; Gaps 5;
 QY 3 LEKIVDAITGDKDKKVKGTIVLMKKNVLDPTDINASVLDGVLEFLGRRVSELEISSVNA 62
 DB 2 LSGIIDGTLGANKHARKLGTIVLMKKNVLDLNDFGATVDSISFELGKGVTCQLISSTLV 61
 QY 63 DPANGLOKRSKAAVLENWLTNSTPIAAGESAFVTFDWDDEEFGVPGAFIINKLHFSEF 122
 DB 62 DANNNGRGRVCAEANLEOWLTISLSTTGSKFGVTFDWEVEKLGVPQAVVKNHAAEF 121
 QY 123 FLKSLTLEDEVNHHGVHCNWSVYVANKYKSDRIFFANQAYLPSETPTTLRKRYRENELV 182
 DB 122 FLKTLTLDVDEGAVTFVANSVYVAGKYRNVFVSNDTYLPSQMPAALKPYRDDBLR 181
 QY 183 TLRGDG-TGKLEWDRVYAYVNDLGDGDKDLSRPVGLGSSEYVPRRGRTRGKPTK 241
 DB 182 NLRGDTGGERKEWERYDYDVNDLGDGDKENHARPVLGNDTFPPRRGRTRGKPTK 239
 QY 242 TDPNSERIPILMSLDIYVPRDERFGHKLSDFLTPALKSIYQLLPEPKALFDSTHNEF 301
 DB 240 TDPNSDSRLSVE--QIYVPRDERFGHKLSDFLGYSIKAITQGIIPAVRYVDTTPGEF 297
 QY 302 DSFEDVLKVEGGIKLPGQLLKAITDSIPILEILKELLSDDGGLFKYPTPQVIOEDKTA 361
 DB 298 DSFQDIINLYEGGIKLPKIQALEDMRKLFPQLVKDLLPAGGDVLLKLPFIQIIQEDKNA 357
 QY 362 WRTEDEFGREMLAGVNPVIISRLQEPPEPKSLDPKLYGNQNSTITREQIEDKLDLTIDE 421
 DB 358 WRTEDEFAREVLAGVNPVITRLTEFPPEPKSLDPSKYGDHTSTITAEHIEKNLEGLTVQQ 417
 QY 422 AIKTNRLFILNHRDILMPYLIRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDG 481
 DB 418 ALDGNRLYLDHHRFVDFIDVNNLEGNFIYATRTLEFLRGDGLAPLAELESPYIDG 477
 QY 482 DOFGAVSKVYTPADQGVESIWQAKAYAAVNDSGVHQLISHWLNTHAAIEPFIATNRQ 541
 DB 478 DLTVAKSVMYTPASSGVAEAWVQAKAYVAVNDSGVHQLVSHWLNTHAVMEPFIATNRQ 537
 QY 542 LSALHPYKLLHPRFETMINALARQILINGGLLELTVFPKYSMEASVYVKNWVFP 601
 DB 538 LSVTHPVKLLSSSHFRDFTMTINALARQILINGGIFEMTVFPGKALGMSVYVKNWFT 597
 QY 602 EOALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKWTEYCNYYKSD 661
 DB 598 EQGLPADLVKGVAVADPSSPKYKVLIEDYFASDGLAIWHAIEQWGEVYLAIYYPDDG 657
 QY 662 AVQKDTLOAWKELBEHGDGKDEFPWPKMOTVQELIDSCTITWIASALHAAVNFQ 721
 DB

Db 658 ALRGDEELQAWKKEVREVGHDHDKADPWWPKMQAVSELASACTTIWIASALHAAVNFQ 717
 QY 722 YPAGYLPNRPRLSRNFMPEPGSPVEELKTNPKVFLKTTIPOLQTLGIGLSILSLSH 781
 Db 718 YPAGYLPNRPVSRNFMPEPGSPVEELKTNPKVFLKTTIPOLQTLGIGLSILSLSH 777
 QY 782 SSDDLVLGQRESPEWTKDQEPISAFARFGKLSLSDIEDQIMQNVDEKWKNSGPKVPYPT 841
 Db 778 SSDEVILGQRTPEWTSARALAAFKRFSALVKIEGKVGNGVGNRDPQLNRNGPAEFFPYM 837
 QY 842 LLFP-TSE-----GGLTGKIPNSVSI 862
 Db 838 LLYPNTSDHSGAAAGLTAKGIPNSISI 864
 RESULT 10
 ADG93379
 ID ADG93379 standard; protein; 864 AA.
 AC ADG93379;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Maize lipoxigenase (LOX) polypeptide #5.
 XX
 KW Maize; lipoxigenase; LOX; corn; plant; plant pathogen defence system;
 KW plant development; tissue healing; mycotoxin; aflatoxin;
 KW sterigmatocystin.
 XX
 OS Zea mays.
 XX
 PN US2003166855-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 25-APR-2002; 2002US-00132350.
 XX
 PR 27-APR-2001; 2001US-0286889P.
 PR 13-JUL-2001; 2001US-0305366P.
 XX
 XX (PION-) PIONEER HI-BRED INT INC.
 XX
 XX Navarro Acevedo PA, Duwick JP, Koloniets MV, Simmons CR;
 XX
 XX WPI; 2003-898106/82.
 DR N-PSDB; ADG93378.
 XX
 XX New lipoxigenase polypeptides and polynucleotides, useful for enhancing
 PT resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for
 PT promoting healing of damage tissues, or for modulating plant growth and
 PT development.
 XX
 PS Disclosure; SEQ ID NO 10; 151pp; English.
 XX
 CC The invention relates to maize lipoxigenase (LOX) polypeptides and
 CC polynucleotides encoding the polypeptides. The LOX polypeptides and
 CC polynucleotides are useful in modulating plant pathogen defence systems
 CC (particularly enhancing resistance to fungi, viruses, nematodes and
 CC insects) and plant development, and for promoting healing of damaged
 CC tissues. LOX proteins may also be used to inhibit the production of
 CC mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing
 CC fungus in plants susceptible to contamination by the mycotoxins. This
 CC sequence represents a maize LOX polypeptide of the invention.
 XX
 SQ Sequence 864 AA;
 Query Match 61.1%; Score 2769.5; DB 7; Length 864;
 Best Local Similarity 60.4%; Pred. No. 8.4e-230;
 Matches 524; Conservative 124; Mismatches 208; Indels 11; Gaps 5;
 QY 3 LEKIVDAITGKDDGKKVGTGTVLKKVNLDFDIDINASVLDGVLGFLGRVSLIELISSVNA 62
 Db 2 LSGIIDGLTGANKHARKVGTGTVLKKVNLDFDIDINASVLDGVLGFLGKVTQLISSTLV 61

QY 63 DPANGLOGKRKAAAYLENWLTNSTPIAAGSAFRVTFDWDEEGVPGAFIINKLHFSF 122
 Db 62 DANNGRGRVGAANLEQWLTSLTTSKESFGVTFDWEVEKLGVPAGVAVVNNHAEF 121
 QY 123 FLKSLTLEDPNKGKHFVFCNWSVYPANKYKSDRIFFAQAYLPSETPTDLKRYRENEVL 182
 Db 122 FLKTLTLDVPGAGAVTEVANSVYPAGKYRNVFFSNDTYLPSQMPAALPYRDEELR 181
 QY 183 TLRGDG-TGKLEEDRVYDAYVNDLGPDPKQDLSRPVLGGSSEYPPRRGRTGRKPK 241
 Db 182 NLRGDDQGPYQEHDRVRYDYNDLGPDPGN--PRPILGGSADHPYRRGRTGRKPK 239
 QY 242 TDPNSESRIPLMSLDIYVPRDEREGHKLSDFTLFAKLSIVQLLPPFKALFDSHNEF 301
 Db 240 TDPNDSRLSLVE--QIVVPRDEREGHKLMSDFLGYSIKATQGIIPAVRTVDTTPGEF 297
 QY 302 DSFEDVLKYEGLIKLPGPLLKAITDSIPLEILKELRSDEGLFKYPTPOVIEDKTA 361
 Db 298 DSFQDIINLYEGGIKLPKIQALEDMRKLPLQLVLDLLPAGGDYLLKLPQIIQEDKNA 357
 QY 362 WRTDEEFGREMLAGUNPVIISRLQEPFKSLDKPKIYGNQNSTITREQIEDKLDGLTIDE 421
 Db 358 WRTDEEFAREVLAGVNPVITLTFEPFKSLDPSKYGDHSTITTAHIEKLNLEGLTVQ 417
 QY 422 AIKTNRFLNHHDIIMPYLRRINTSTDTKTVASRTLLFLODNGTLKPSAIELSLPHPDG 481
 Db 418 ALDGNRLYLDHDBFMFLDVNNLEGNFIYATLTFLLRGDGRAPLAPLSESPYIDG 477
 QY 482 DQFQAVSKVYTPADQGVESISWQLAKAYAVANDSGVHOLISHLNTAAIEPFVIATNRQ 541
 Db 478 DLTVAKSKVYTPASSGVEAWVQLAKAYAVANDSGVHQLVSHLNTAAVMEPFVIATNRQ 537
 QY 542 LSAHPYIKLHPHRETNNALARQILNGGELLELTVPKYSMEMSAVYKDWFP 601
 Db 538 LSVTHPVHKLSSHFRDNTNALARQTLNGGGIFEMTVFGKVALGMSVYKSWNFT 597
 QY 602 EOALPTDLIKRGVAVEDSSPLGIRLLIODYPYAVDGLKIWSAISKSWTEYCNYYKSD 661
 Db 598 EQGLPADLVKGVAVADPSLYKVRLLIEDIPYASDGLAIWHAIEQWGEYLAIYYPDG 657
 QY 662 AVQKDELQAWKELREHGDKKDEPMPKQVQVELIDSCITITITIASALHAAVNFQ 721
 Db 658 ALRGDEELQAWKKEVREVGHDHDKADPWWPKMQAVSELASACTTIWIASALHAAVNFQ 717
 QY 722 YPAGYLPNRPRLSRNFMPEPGSPVEELKTNPKVFLKTTIPOLQTLGIGLSILSH 781
 Db 718 YPAGYLPNRPVSRNFMPEPGSPVEELKTNPKVFLKTTIPOLQTLGIGLSILSH 777
 QY 782 SSDDLVLGQRESPEWTKDQEPISAFARFGKLSLSDIEDQIMQNVDEKWKNSGPKVPYPT 841
 Db 778 SSDEVILGQRTPEWTSARALAAFKRFSALVKIEGKVGNGVGNRDPQLNRNGPAEFFPYM 837
 QY 842 LLFP-TSE-----GGLTGKIPNSVSI 862
 Db 838 LLYPNTSDHSGAAAGLTAKGIPNSISI 864
 RESULT 11
 ADG93381
 ID ADG93381 standard; protein; 864 AA.
 XX
 AC ADG93381;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Maize lipoxigenase (LOX) polypeptide #6.
 XX
 KW Maize; lipoxigenase; LOX; corn; plant; plant pathogen defence system;
 KW plant development; tissue healing; mycotoxin; aflatoxin;
 KW sterigmatocystin.
 XX
 OS Zea mays.


```
QY 115 KNLHSEFLKSLTLEDVPHKGVHVCNSVVPANKYKSDRIEFANOAYLPSETPTDLR 174
Db 120 RNLOHAEFFLKLTLGVPVGGTVVFNANSVPHNLYSQERVFANDTYLPSKMPAAVLV 179
QY 175 KYRENELVLRG-DGTGKLEWDRVYDYAYNDLGDGDPKQDLSPVLGSGSEYPPRRG 233
Db 180 PYRQDELKILAGDDNPGPYKEHDRVYDYNDLGEPPKGDHARPVLGSGQEHYPYPRC 239
QY 234 RTGRKPTKTDNPSSESRIPLLMSLDIYVPRDRFGHIKLSDFLTALKSIVOLLIPFKAL 293
Db 240 RTGRPTETDPSSESRLL-FLNLNIYVPRDRFGHLKMSDFLGYSLKAIIEAVLPTLGRF 298
QY 294 FDSITHNEFDSFEDVLKLYEGGKILPQGPLLKAITDSIPLEILKELLRSDG--EGLFKYPT 351
Db 299 VDDTPKFDSFEDILGLYEPGPEAPNNPLVAEVRKRIPESEFLRSIL-PDGSHDHPLKMP 357
QY 352 PQVIOED-----KTAWRTDEEFGREMLAGVNPVVISRLQEFPPKSLDPKPIYGNQNS 403
Db 358 PNIIRSDVLKKAPEKFCGWRTEDEFARETLAGVNPVLIKRLTEPAKSTLDPSQYGDHTS 417
QY 404 TITREIQEDKLDGLTIDBAIKTNRLFILNHHDLIMPYLRINTSTDTTKYASRTLLFLOD 463
Db 418 KITEAHIOHNEGLSVQNALKNRFLILDHDFHFWPYNLKNINELEGNFIYASRTLLFLKD 477
QY 464 NGLTKPSAIELSLPHDPDQFGAVSKVYTPADQGVGSIWOLAKAYAAVNDGSGVHQLISH 523
Db 478 DGTLLKPLAVELSLPHDPDQGGQGVAVSKVYTPAHSGABGHVWOLAKAYACVNDAMHQLISH 537
QY 524 WLNTAAIEPFIATNRQLSALHPIYKLLHPHFRETMINALARQILINGGGLLELTVP 583
Db 538 WLNTHAVIEPFIATNRQLSVHPVHKLLSPHYRDTLNALARQTLINADGIFERTVFP 597
QY 584 AKYSMEMSAVVYKOWFPEQALPTDLIKRGVAVEDSSPLGIRLLIODYPYAVDGLKIWS 643
Db 598 AKYALGMSDDVYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPYAVDGLVIW 657
QY 644 AIKSWVTCYCNYYKSDDAVOKDTELOAWKELREEGHDKDEPMPKMTQVLELIDSC 703
Db 658 ALERWVKYLDVYNDGELQDLQLOAWKEVREEAHGDKLDKRDWPRMDAVQRLARAC 717
QY 704 TITWIASALHAANFGQYPYAGYLPNRPPLSRNFMPEPPGSPYBELKT--NPDKVLK 760
Db 718 TTVIVASALHAANFGQYPYAGYLPNRPVSRPMPPEGSDDYKLEAGQKEADAVIR 777
QY 761 TITPOLQTLIGLSLIEILSRHSDTYLIGORESPE-WTKDQEPPLSAFAPFGKLSIDEDQ 819
Db 778 TITTSQFOTILGISLIEILSKHSDSVYLQORDEPERWTSARALDAFRFRGSLVEIEKR 837
QY 820 IMQNVNDEKKNRSGPVKVPYTLLEPTSEG-----GLTGKGIPINSVI 862
Db 838 IRTMNDSPTLKNRKGPEVMPYMLLYPNTSDVTGKGEGLTAMGIPNSISI 887

RESULT 14
ADG93387
ID ADG93387 standard; protein; 887 AA.
XX AC
XX ADG93387;
XX DT
XX 11-MAR-2004 (first entry)
XX DE
XX Maize lipoxigenase (LOX) polypeptide #9.
XX Maize; lipoxigenase; LOX; corn; plant; plant pathogen defence system;
KW plant development; tissue healing; mycotoxin; aflatoxin;
XX sterigmatocystin.
XX OS
XX Zea mays.
XX PN
XX US2003166855-A1.
XX PD
XX 04-SEP-2003.
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XX 25-APR-2002; 2002US-00132350.
XX 27-APR-2001; 2001US-0286889P.
PR 13-JUL-2001; 2001US-0305366P.
XX (PION-) PIONEER HI-BRED INT INC.
XX Navarro Acevedo PA, Duvick JP, Kolomiets MV, Simmons CR;
XX WPI; 2003-898106/82.
DR N-PSDB; ADG93386.
XX New lipoxigenase polypeptides and polynucleotides, useful for enhancing
PT resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for
PT promoting healing of damage tissues, or for modulating plant growth and
PT development.
XX Claim 1; SEQ ID NO 18; 151pp; English.
XX The invention relates to maize lipoxigenase (LOX) polypeptides and
XX polynucleotides encoding the polypeptides. The LOX polypeptides and
XX polynucleotides are useful in modulating plant pathogen defence systems
XX (particularly enhancing resistance to fungi, viruses, nematodes and
XX insects) and plant development, and for promoting healing of damaged
XX tissues. LOX proteins may also be used to inhibit the production of
XX mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing
XX fungus in plants susceptible to contamination by the mycotoxins. This
XX sequence represents a maize LOX polypeptide of the invention.
XX Sequence 887 AA;
XX Query Match 60.3%; Score 2734.5; DB 7; Length 887;
XX Best Local Similarity 59.6%; Pred. No. 9.4e-224;
XX Matches 530; Conservative 115; Mismatches 217; Indels 31; Gaps 11;
QY 1 MFLEKIVDAITGKD----DGKKVGTGTVLMKKNVLDFTDINASVLGDGVLEFLG--RRVSL 54
Db 1 MFWHGVAADRLTGKKEANEKGIKGTVRLVKEVLDVGDVFNASLLDGVHRLGWDGVA 60
QY 55 ELISSVNADPANGLOGKRSKAAYLENMLTNSPTAAGESAPRVTFDWDDEFFGVPGAFII 114
Db 61 QLVSAATAADPNSGRGKVGKAAHLEAEAVSLKSTTDTGETVYRVSPFWDGSGQ-GVPGAVLV 119
QY 115 KNLHSEFLKSLTLEDVPHKGVHVCNSVVPANKYKSDRIEFANOAYLPSETPTDLR 174
Db 120 RNLOHAEFFLKLTLGVPVGGTVVFNANSVPHNLYSQERVFANDTYLPSKMPAAVLV 179
QY 175 KYRENELVLRG-DGTGKLEWDRVYDYAYNDLGDGDPKQDLSPVLGSGSEYPPRRG 233
Db 180 PYRQDELKILAGDDNPGPYKEHDRVYDYNDLGEPPKGDHARPVLGSGQEHYPYPRC 239
QY 234 RTGRKPTKTDNPSSESRIPLLMSLDIYVPRDRFGHIKLSDFLTALKSIVOLLIPFKAL 293
Db 240 RTGRPTETDPSSESRLL-FLNLNIYVPRDRFGHLKMSDFLGYSLKAIIEAVLPTLGRF 298
QY 294 FDSITHNEFDSFEDVLKLYEGGKILPQGPLLKAITDSIPLEILKELLRSDG--EGLFKYPT 351
Db 299 VDDTPKFDSFEDILGLYEPGPEAPNNPLVAEVRKRIPESEFLRSIL-PDGSHDHPLKMP 357
QY 352 PQVIOED-----KTAWRTDEEFGREMLAGVNPVVISRLQEFPPKSLDPKPIYGNQNS 403
Db 358 PNIIRSDVLKKAPEKFCGWRTEDEFARETLAGVNPVLIKRLTEPAKSTLDPSQYGDHTS 417
QY 404 TITREIQEDKLDGLTIDBAIKTNRLFILNHHDLIMPYLRINTSTDTTKYASRTLLFLOD 463
Db 418 KITEAHIOHNEGLSVQNALKNRFLILDHDFHFWPYNLKNINELEGNFIYASRTLLFLKD 477
QY 464 NGLTKPSAIELSLPHDPDQFGAVSKVYTPADQGVGSIWOLAKAYAAVNDGSGVHQLISH 523
Db 478 DGTLLKPLAVELSLPHDPDQGGQGVAVSKVYTPAHSGABGHVWOLAKAYACVNDAMHQLISH 537
QY 524 WLNTAAIEPFIATNRQLSALHPIYKLLHPHFRETMINALARQILINGGGLLELTVP 583
```

Db 538 WLNTHAVIEPPFIATNRQLSVVHPVHKLSPHYRDTLNALAROTLINADGIFERTVFP 597
Qy 584 AKYSMEMSAVYKDWVPEQALPTDLIKGVAVEDSSPLGIRLAIQDYPYAVDGLKWS 643
Db 598 AKYALGMSDDVYKSNWFNEQALPADLVKRGVAVPDQSSPYGVRLLIKQDYPYAVDGLVIWM 657
Qy 644 AIKSWVTEYCNYYKSDDAVQKDTLQAWWKELBEGHDKDEPWPQKQVQVQELIDSC 703
Db 658 AIERWVKEYLDVYYPNDGELQDVELQAWWKEVREAHGDLKDRWPMQVAVQRLARAC 717
Qy 704 TITIWIASALHAANFGQYPYAGYLPNRPRTLNRNFMPEPGSPYBELKT---NPKVFLK 760
Db 718 TTVIIVASALHAANFGQYPYAGYLPNRPRTVSRNFMPEPGSDYKKEAGQKEADAVFIR 777
Qy 761 TITPOLQTLGLISLIEILSRHSSDTLYLGORESPWTKDQEPISAFARFGKLSIEDQ 819
Db 778 TITPOLQTLGLISLIEILSRHSSDTLYLGORESPWTKDQEPISAFARFGKLSIEDQ 837
Qy 820 IQMNVDEKWKNRSGPVKVPYTLPTPTSEG-----GLTGKGINPSVSI 862
Db 838 IRTWNSPTLKNKRGVEMPYMLLYPNTSDVTGKGEGLTANGIPNSISI 887
RESULT 15
AAO27494
XX AAO27494 standard; protein; 887 AA.
AC AAO27494;
XX
DT 06-NOV-2003 (first entry)
XX
DE Corn (Zea mays) lipoxigenase isozyme 4 amino acid sequence.
XX
KW Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;
KW fatty acid metabolite synthesis; signal molecule; growth regulation;
KW development regulation; plant development; wound response;
KW genetic mapping; hyperoxidation catalysis; Corn; enzyme.
XX
OS Zea mays.
XX
PN US2003074693-A1.
XX
PD 17-APR-2003.
XX
PF 29-JAN-2002; 2002US-00059909.
XX
PR 10-FEB-1999; 99US-0119597P.
PR 09-FEB-2000; 2000US-00501422.
XX
PA (CAHO/) CAHOON E B.
PA (KINN/) KINNEY A J.
PA (KLEI/) KLEIN T M.
PA (LEEJ/) LEE J.
PA (PEAR/) PEARLSTEIN R W.
PA (RAFA/) RAFALSKI J A.
PA (SHEN/) SHEN J B.
PA (THOR/) THORPE C J.
PA (TING/) TINGEY S V.
PA (WENG/) WENG Z.
XX
PI Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;
PI Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;
XX
XX WPI; 2003-567325/53.
DR N-PSDB; AAL57714.
XX
XX New isolated polynucleotides encoding plant lipoxigenases, useful in
XX genetic mapping, particularly in catalyzing hyperoxidation of
XX polyunsaturated fatty acids.
PS Claim 19; Page 29-31; 36pp; English.
XX

CC This invention relates to novel nucleotide sequences which encode
CC proteins which have lipoxigenase activity. Lipoxigenases are membrane
CC bound ubiquitous enzymes which catalyze the hydroperoxidation of
CC polyunsaturated fatty acids in the first step of fatty acid metabolite
CC synthesis. Products of this pathway are found as signal molecules
CC involved in growth and development regulation. A knowledge of the amino
CC acid sequence of lipoxigenases may allow the understanding of plant
CC development and wound response. The polynucleotides, polypeptides and
CC lipoxigenases of the invention may therefore be useful in genetic mapping
CC and particularly for catalyzing hydroperoxidation of polyunsaturated
CC fatty acids. The present sequence is the amino acid sequence of the Corn
CC (Zea mays) lipoxigenase protein 4 of the invention
XX
SQ Sequence 887 AA;
Query Match 60.1%; Score 2724.5; DB 6; Length 887;
Best Local Similarity 59.9%; Pred. No. 6.9e-226;
Matches 533; Conservative 111; Mismatches 215; Indels 31; Gaps 11;
Qy 1 MFLEKIVDAITGKD-----DGKVKGTGTVLMKKNVLDFTDINASVLDGVLFLG--RRVS 53
Db 1 MFWHCVADRLTGKKEAMSEG-KIRGTVRLVKKEVLDVDFDNASLLDGVHRLGLGDDGVA 59
Qy 54 LELISSVNADPANGLOGRKSKAAYLENWLMTSTPTIAGESAFRVTFDWDDBEFVPGAPI 113
Db 60 FQLVSATAADPSNGGRGKVGKAAHLEEAVALKSTADGETVYRVSEFWEDESQ-GIPGAVL 118
Qy 114 IKNLHSEFFLSLTLEDVPHNGKVFVCSNWSVYPAKYSKDRIFPANAQVLPSTPDTL 173
Db 119 VRNLQHAFFLKTLEGVPGKGTGVFVANSWVYPHKLYSOERIFFANDTYLPKMPAAL 178
Qy 174 RKYRENELVTLRG-DTGKLEEDRVYDYAYNDLGDGDKGDLRSPVLGGSEYPPR 232
Db 179 VPYQDELKIIRGDDNPGYQEHDRVYDYNDLGDGDKGEHARPILGSGQEHPPR 238
Qy 233 GRTGRKPTKTPNSESRIPLMSLDIYVPRDERFGHIKLSDFLTALKSIIVOLLPEFKA 292
Db 239 CRTGRHPTKDPNSESRL-FLNLNLYVPRDERFGHLKMSDFLGYSLKATITEAVLPLGT 297
Qy 293 LFDSTHNEFDSFEDVLKLYEGIKLPQGPILKAITDSIPLEILKELL-RSDGEGFLPKPT 351
Db 298 FVDPTPKFDSFEDILGLYELGPEAPNPNPLTAERKKIPSEFLRSLPNSGSHDPLKMP 357
Qy 352 PQVIQED-----KTAWRTDEEFGREMLAGVNPVTSRLQEPFPPKSKLDPKIYGNONS 403
Db 358 PNVIKSDVLKXAPKFKGRTDEEFARTLAGVNPVTKRLTEFPKXSTLDPQYGDHTS 417
Qy 404 TITREQIEDKLDGLTIDEAINKRLFILNHHDIILMPYLRRINTSTDTKTYASRTLLFLQD 463
Db 418 KITEAHIRHNMGGLSVQNALRNKRLFILDHDFMPYLDINELEGNFIYASRTLLFLKD 477
Qy 464 NGTLKPSAIELSLPHPDGQFGAVSKVYTPADQGVGSIWOLAKAYAAVNDSGVHQLISH 523
Db 478 DGTLLKPLAIELSLPHPDGQQRGAVSKVYTPARTGVGHHVQWLAKAYACVNDSSAMHQLISH 537
Qy 524 WLNTHAAJEPFVIATNRQLSALHPIYKLLPHFRBTMINALAROLINGGGLLELTVP 583
Db 538 WLNTHAVIEPPFIATNRQLSVVHPVHKLSPHYRDTLNALAROTLINAGGVFERTVFP 597
Qy 584 AKYSMEMSAVYKDWVPEQALPTDLIKGVAVEDSSPLGIRLAIQDYPYAVDGLKWS 643
Db 598 AKYALGMSADVYKSNWFNEQALPADLVKRGVAVPDQSSPYGVRLLIKQDYPYAVDGLVIWM 657
Qy 644 AIKSWVTEYCNYYKSDDAVQKDTLQAWWKELBEGHDKDEPWPQKQVQVQELIDSC 703
Db 658 AIERWVKEYLDIYYPNDGELQDVELQAWWKEVREAHGDLKDRWPMQVAVQRLARAC 717
Qy 704 TITIWIASALHAANFGQYPYAGYLPNRPRTLNRNFMPEPGSPYBELKT---KTNPKVFLK 760
Db 718 TITIWIASALHAANFGQYPYAGYLPNRPRTVSRNFMPEPGSDYKKEAGQKEADAVFIR 777
Qy 761 TITPOLQTLGLISLIEILSRHSSDTLYLGORESPWTKDQEPISAFARFGKLSIEDQ 819

Db 778 TITSQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENR 837
Qy 820 IMQNNVDEKWKNRSGPVKVPYTLLEPTSEG-----GLTGKGIENSYSI 862
Db 838 IKTWNDSPLKNRKGPVEMPYNLLYPNTSDVTGKAEGLTAMGIPNSISI 887

Search completed: March 10, 2005, 18:59:00
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:56:07 ; Search time 149 Seconds
(without alignments)
1908.230 Million cell updates/sec

Title: US-10-731-642A-1

Perfect score: 4534

Sequence: 1 MFLEKIVDAITGDKDGKKVK.....LPFTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3610	79.6	859	10	US-09-978-522-3
2	3576	78.9	862	10	US-09-978-522-1
3	3346.5	73.8	887	15	US-10-425-114-54449
4	3104.5	68.5	864	15	US-10-425-114-46828
5	3090	68.2	859	15	US-10-424-599-213159
6	3022.5	66.7	880	14	US-10-059-909-12
7	2909	64.2	857	15	US-10-424-599-215976
8	2909	64.2	860	15	US-10-425-114-45769
9	2909	64.2	863	15	US-10-425-114-54429
10	2909	64.2	863	15	US-10-425-114-55253
11	2905	64.1	857	10	US-09-751-687-17
12	2849.5	62.8	826	15	US-10-424-599-215973
13	2849.5	62.8	832	15	US-10-425-114-45631

14	2791.5	61.6	888	16	US-10-437-963-165232	Sequence 165232,
15	2790	61.5	860	15	US-10-424-599-220216	Sequence 220216,
16	2769.5	61.1	864	14	US-10-132-350-10	Sequence 10, Appl
17	2769.5	61.1	864	14	US-10-132-350-12	Sequence 12, Appl
18	2763.5	61.0	871	15	US-10-425-114-62385	Sequence 62385, A
19	2765.5	60.8	865	15	US-10-424-599-258944	Sequence 258944,
20	2754	60.7	866	15	US-10-424-599-239573	Sequence 239573,
21	2745.5	60.6	865	10	US-09-751-687-16	Sequence 16, Appl
22	2734.5	60.3	887	14	US-10-132-350-18	Sequence 18, Appl
23	2734.5	60.3	887	14	US-10-132-350-20	Sequence 20, Appl
24	2733.5	60.3	926	15	US-10-425-114-69756	Sequence 69756, A
25	2730.5	60.2	866	16	US-10-437-963-116093	Sequence 116093,
26	2727	60.1	786	15	US-10-425-114-46295	Sequence 46295, A
27	2724.5	60.1	887	14	US-10-059-909-16	Sequence 16, Appl
28	2724.5	60.1	887	14	US-10-132-350-22	Sequence 22, Appl
29	2724.5	60.1	887	14	US-10-132-350-24	Sequence 24, Appl
30	2704	59.6	881	15	US-10-425-114-57754	Sequence 57754, A
31	2704	59.6	882	15	US-10-425-114-54555	Sequence 54555, A
32	2704	59.6	964	16	US-10-437-963-141895	Sequence 141895,
33	2700.5	59.6	873	14	US-10-132-350-2	Sequence 2, Appli
34	2700.5	59.6	873	14	US-10-132-350-4	Sequence 4, Appli
35	2700.5	59.6	891	15	US-10-425-114-62915	Sequence 62915, A
36	2700	59.6	868	15	US-10-424-599-242598	Sequence 242598,
37	2699	59.5	856	15	US-10-424-599-151512	Sequence 151512,
38	2694.5	59.4	853	15	US-10-424-599-151510	Sequence 151510,
39	2694.5	59.4	860	15	US-10-425-114-39867	Sequence 39867, A
40	2694.5	59.4	862	15	US-10-425-114-42418	Sequence 42418, A
41	2694.5	59.4	863	15	US-10-425-114-39883	Sequence 39883, A
42	2694.5	59.4	863	15	US-10-425-114-47348	Sequence 47348, A
43	2694.5	59.4	865	15	US-10-425-114-40151	Sequence 40151, A
44	2694.5	59.4	866	15	US-10-425-114-40047	Sequence 40047, A
45	2694.5	59.4	867	15	US-10-425-114-39889	Sequence 39889, A

ALIGNMENTS

RESULT 1

US-09-978-522-3
; Sequence 3, Application US/09978522
; Publication No. US20030033627A1
; GENERAL INFORMATION:
; APPLICANT: Descenzo, Richard
; APPLICANT: Irelan, Nancy
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera
; FILE REFERENCE: 29520/37890
; CURRENT APPLICATION NUMBER: US/09/978,522
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,220
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Vitis LOX 2
US-09-978-522-3

Query Match 79.6%; Score 3610; DB 10; Length 859;
Best Local Similarity 76.9%; Pred. No. 1.3e-285;
Matches 661; Conservative 106; Mismatches 91; Indels 2; Gaps 2;

Qy	3	LEKIVDAITGDKDGKKVGTVMKKNVLDFTDINASVLDGVLEPLGRRVSLLEISSVNA	62
Db	2	IHSIVGAITGENDKKIKGTVMKKNVLDNFNFNASVLDGVLEPLGRRVSLLEISSVNA	61
Qy	63	DPANGLOKRSKAAVLENLWNTNSPIAAGESAFRTVFDWDEEFGVPCAFITKILHFSEF	122
Db	62	DPANGLOKIKPAYLEDWITITISLTAGESAFKVTFW-DEEIGEPQAFIRNNHSEF	120
Qy	123	FLKSITLEDVFNHGKHFVFCNCSWVYPANKYKSDRIFFANQAYLPSETPTLTKYRENLV	182
Db	121	YLRTITLEDVFGRIHFVFCNCSWVYPQAHYKTDRAVFTNTQYLPSETPGPLRKYREGLV	180


```

/ APPLICANT: Kovacic, Steven E.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Methods of Plant Improvement
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 46828
/ LENGTH: 864
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 701040644_FLI.pep
US-10-425-114-46828

Query Match      68.5%; Score 3104.5; DB 15; Length 864;
Best Local Similarity 67.8%; Pred. No. 2.8e-244;
Matches 578; Conservative 123; Mismatches 133; Indels 13; Gaps 8;

QY      17 KKVGTVLMLKKNVLDFTDINASVLDGVLEFLGRRVSVLELISVNADPADNGLQKSKAA 76
DB      18 KRVGREVLMLKGVLD FHD I KANVLDRVHLLGKGVSLQLISATTPDPAGKL--LRKVA 75

QY      77 YLENMLTNTPTI--AGESAFRVTFDWDDEEFGVPGAFIINKLHFSBEFFKSLTLEDVPH 135
DB      76 NLERWVSTITSLTSTDTDETSVTFEW--DESMGVPGAFIIRNNHHSQFYKLTLTIEDIPGH 134

QY      136 -GKVFVNCNWSYPANKYKSDRIEFANQAVLQSETPTDILRKYRENEVLTLRGDGTGKLE 194
DB      135 DGVNPFVNCNWSYPAHRYAHDVRFVANKAYLPCHTPEPLRKFREQELKTLGCGFGOKLNE 194

QY      195 WDRVVDYAYNDLGDGPKQDLSRPLVGSSSYPYPRRGTRGRKPTKTDPNSESRIPLLM 254
DB      195 WDRVVDYAYNDLGLDGDGPDYARPVLG--SQFPYPRRGTRSRPHCKTDPKTESRLHLL-- 252

QY      255 SLDDIVYPRDERFGHIKLSDFLTFALKSVIQLLLPEPKALFDSTHNEFDSFEDVLKLYEGG 314
DB      253 NLNVVYPRDEQFGHVKFSDFLAYSLSKVAQVLLPEIKSLCDKKTINEFDTFQDVLDIYEGS 312

QY      315 IKLPGPGLLKAITDSIPLRIKELLRSDCGELFKYPTPOVIQEDKTAWRTDEEFGREMLA 374
DB      313 IKLPGSGLTSKLKRVLYPELLRELIKNDGERFLKFPVPDVIKVSKTAWRTDEEFAREMLA 372

QY      375 GNPVLIISRLQFPFKSKLDPRYIGNQNSNTITREQTEDKLDGLTIDEAIKTNRLFIINHH 434
DB      373 GNPVLIIRLQFPFPASKLDPSVYGDQTSIRATHIENSRLDGLTIDEAIGNMELFILDHH 432

QY      435 DILMPYLRRINTSTDTKTVASRTLLFLQNGTILKPSAIELSLPHPPDGDQFGAVSKYVTPA 494
DB      433 DSLMPYIISRIN--STNTKTVASRTLLFLQDDGTILKPLAIELSLPHPPQGEHGAVSKYVTPA 491

QY      495 DQGVESGIWQAKAVAAVNDSGVHQLISHWLNTAAIEPFLVATNRPQLSALHPDIYKLLHP 554
DB      492 QGVGSASVWQAKAVAAVNDSGVHQLVSHWLTVHVEIPFIATNRPQLSLTHPIHKLLKP 551

QY      555 HFRETWNINALARQILINGGGLELTLTVFPKATYSMEMSAVVYKDWVPPEQALPTDLIKRGV 614

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Query Match      66.7%; Score 3022.5; DB 14; Length 880;
Best Local Similarity 65.4%; Pred. No. 14e-237;
Matches 554; Conservative 132; Mismatches 156; Indels 5; Gaps 4;

QY 16 GKXVGTVMKQVLDFTDINASVLDGVLEFLGRVSLSSVADNANGKGRSKA 75
Db 39 GKXVGTVMKQVLDFTDINASVLDGVLEFLGRVSLSSVADNANGKGRSKA 75
QY 76 AVLENLWLTSTPAAGSAFRVTFDWDDEFGVPGAFIKNLHFSFELSLTLEVPNH 135
Db 97 ALEWLTLSTPAAGSAFRVTFDWDDEFGVPGAFIKNLHFSFELSLTLEVPNH 135
QY 136 GKXVHFCVSNWYVANKYKSDRIFFANQAYLPSTPTDLAKYRENEVLTLRGDGTGLEW 195
Db 156 GRVHFCVSNWYVANKYKSDRIFFANQAYLPSTPTDLAKYRENEVLTLRGDGTGLEW 195
QY 196 DRYDYAYVNDLGDPPKQODLGRVPGVSGSEVYPPRRGRTKPTKDPNSRSRPLIMS 255
Db 216 DRYDYVNDLGDPPKQODLGRVPGVSGSEVYPPRRGRTKPTKDPNSRSRPLIMS 255
QY 256 LDIVYPRDERFEGHILKSLDELTPALKSIQVLLPPEFKALFDSSTHNEPDSFEDVLKLYEGGI 315
Db 276 LNIYPRDERFEGHILKSLDELTPALKSIQVLLPPEFKALFDSSTHNEPDSFEDVLKLYEGGI 315
QY 316 KLPOGPLLKAITDSIPLEILKELLRSDGEGFLFKYPTTQVIOEDKTAWRTDEEFGREMLAG 375
Db 336 PIPLN-IFKNLTEDLAPFLKAFRLSDGERFLKYPTTQVIOEDKTAWRTDEEFGREMLAG 375
QY 376 VNPVIISRLQEPFPPKSLDPKPYGNQNSTITREIQEDKLDGLTIDRAIKNRLFLINHHDD 435
Db 395 VNPVIIRLEVPFPLSKLDPHYVGNQNSTITREIQEDKLDGLTIDRAIKNRLFLINHHDD 435
QY 436 ILMPYLRLNTSDTKYASRLLFLQDNGTLKPSAIELSLPHPDGQDQGVASKVYTPAD 495
Db 455 ALMPYLRLN-STSTKYATRLFLKQDSTLKLPLAIELSLPHPDGQDQGVASKVYTPAD 495
QY 496 QGVESGIWQAKAYAAVNDGSHQLSHWLNTHAAIEPPVIATNROLSALHPYIKLLHPH 555
Db 514 GRVESAIWQAKAYAAVNDGSHQLSHWLNTHAAIEPPVIATNROLSALHPYIKLLHPH 555
QY 556 PRETNINARQILINGGLLELTVFPKAKYSEMSAVVYKDWVPEQALPTDLIKRGVA 615
Db 574 KYDTWFINASARQILINAGGLLELTVFPKAKYSEMSAVVYKDWVPEQALPTDLIKRGVA 615
QY 616 VEDSSPIGIRLLIQDYPAVADGLKIWSAKWVTEYCNYYKSDDAVQKDTLOQAWKE 675
Db 634 IDSGSPHGVRLINDYPPAVDGLKIWSAKWVTEYCNYYKSDDAVQKDTLOQAWKE 675
QY 676 LREEGHGDKDEPWPMPKMTVOELDISCTITTIWASALHAANFGQYVAGYLPNRPPLS 735
Db 694 LREKHTDKDEPWPMPKMTVOELDISCTITTIWASALHAANFGQYVAGYLPNRPPLS 735
QY 736 RNFMPPEGSPEYELKTNPKVFLKTTITPQLOTLGLISLIELSRHSSDTLYLGRESPE 795
Db 754 RNFMPPEGSPEYELKTNPKVFLKTTITPQLOTLGLISLIELSRHSSDTLYLGRESPE 795
QY 796 WTKDEPLSAPARFGKSLSDIEDQIMQMVNDKWKRSQVYPTLLPPTSEGGTLGKG 855
Db 814 WTKDEPLSAPARFGKSLSDIEDQIMQMVNDKWKRSQVYPTLLPPTSEGGTLGKG 855
QY 856 IPNSVSI 862
Db 874 IPNSVSI 880

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RESULT 7

US-10-424-599-215976
; Sequence 215976, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 215976
LENGTH: 857
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_37056C.1.pap
US-10-424-599-215976

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Query Match      64.2%; Score 2909; DB 15; Length 857;
Best Local Similarity 63.4%; Pred. No. 2.6e-228;
Matches 549; Conservative 122; Mismatches 159; Indels 36; Gaps 9;

QY 16 GKXVGTVMKQVLDFTDINASVLDGVLEFLGRVSLSSVADNANGKGRSKA 62
Db 9 GHKIKGTVMKQVLDFTDINASVLDGVLEFLGRVSLSSVADNANGKGRSKA 68
QY 63 DPANGLOQKRSKAAYLENLWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFSBF 122
Db 69 D-ANG-KGKLKATFLEGIITSLPTLGAQSAFKINFWDGSG-GIPGAFYIKNFMQTEF 125
QY 123 FLKSLTLEDPVNHGKVFVCSNWWYVANKYKSDRIFFANQAYLPSTPTDLAKYRENEVL 182
Db 126 FLVSLTLEDPVNHGKVFVCSNWWYVANKYKSDRIFFANQAYLPSTPTDLAKYRENEVL 185
QY 183 TLRGDGTGKLEMDVYVAYVNDLGDPPKQODLGRVPGVSGSEVYPPRRGRTKPTK 242
Db 186 NLRGDTGERKEWERYDYVYNDLGDPPKQODLGRVPGVSGSEVYPPRRGRTKPTK 245
QY 243 DPNSRSRPLIMSLLDIYVPRDERFEGHILKSLDELTPALKSIQVLLPPEFKALFD--STHNE 300
Db 246 DPNSRSR-----SNDVYLPDEAFGLKSSDPLTYGLKSVSONVLPLOSADFNLFTPRE 300
QY 301 FDSFEDVLKLYEGGILKPOGPLLKAITDSI-----PLEILKELLRSDGEGFLKYPTTQVIO 356
Db 301 FDSFEDVHLYSGGILKPL-----TDIISKISPLVPLKEIFRTDGEQALFPPPKVIO 352
QY 357 EDKTAWRDDEEGRMLAGVNPVILSRLOEPFPPKSLDPKPYGNQNSTITREIQEDKLOG 416
Db 353 VSKSAMWTDDEEPAREMLAGVNPVILSRLOEPFPPKSLDPKPYGNQNSTITREIQEDKLOG 412
QY 417 LTIDEAIKTNRLFIINHHDIILMPYLRLNTSDTKYASRLLFLQDNGTLKPSATELSL 476
Db 413 LTIDEAIKTNRLFIINHHDIILMPYLRLNTSDTKYASRLLFLQDNGTLKPSATELSL 471
QY 477 PHPDGQDQGVASKVYTPADQGVESGIWQAKAYAAVNDGSHQLSHWLNTHAAIEPPVI 536
Db 472 PHPDGQDQGVASKVYTPADQGVESGIWQAKAYAAVNDGSHQLSHWLNTHAAIEPPVI 531
QY 537 ATNROL-SALHPYIKLLHGFRETNINARQILINGGLLELTVFPKAKYSEMSAVVYK 596
Db 532 ATNRLHSVVHPYIKLLHGFRETNINARQILINGGLLELTVFPKAKYSEMSAVVYK 591
QY 597 DWVFEQALPTDLIKRGVAVEDSSSPLGIRLLIOQYPAVADGLKIWSAKWVTEYCNYY 656
Db 592 DWVFEQALPTDLIKRGVAVEDSSSPLGIRLLIOQYPAVADGLKIWSAKWVTEYCNYY 651
QY 657 YKSDDAVQKDTLOQAWKEKDEPWPMPKMTVOELDISCTITTIWASALHAANFGQYVAGYLPNRPPLS 716
Db 652 YKSDDAVQKDTLOQAWKEKDEPWPMPKMTVOELDISCTITTIWASALHAANFGQYVAGYLPNRPPLS 711
QY 717 VNFQGYPAVAGYLPNRPPLS RNFMPPEGSPEYELKTNPKVFLKTTITPQLOTLGLISLIE 776
Db 712 VNFQGYPAVAGYLPNRPPLS RNFMPPEGSPEYELKTNPKVFLKTTITPQLOTLGLISLIE 771
QY 777 ILRSRSDTLVYLGQRESPEWTKDQPLSAFARFGKSLSDIEDQIMQMVNDKWKRSQVYPTLLPPTSEGGTLGKG 836

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Db 772 ILSRSHASDEVILGERDNEWTSDTRALEAFKRFNGKLAQIENKLSERNNDKLRNCGPV 831
Qy 837 KVPYTLPTSEGGLTGKIPNSVSI 862
Db 832 QMPYTLPLPSKGLTFRGIPNSISI 857

RESULT 8
US-10-425-114-45769
; Sequence 45769, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45769
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700675903_FLI.pep
US-10-425-114-45769

Query Match 64.2%; Score 2909; DB 15; Length 860;
Best Local Similarity 63.4%; Pred. No. 2.6e-228;
Matches 549; Conservative 122; Mismatches 159; Indels 36; Gaps 9;

Qy 16 GKVKGTWLMKKNVLDFT-----DINASVLDGVLEFLGRVSLLEISSVNA 62
Db 12 GHKIGTIVLMKKNVLDVNSVTSVGGIIGQGLDVGSTLDTLTAFLGRSVLSLQISATKA 71

Qy 63 DPANGLOKRSKAAAYLENLWNTSTPIAAGESAFRVTDFWDDDEEFGVGFATIKNLHFSEF 122
Db 72 D-ANG-KGKLGKATFLEGIITSLPTLGAGSAFKNFEMDDGS-GIPGAFYIKNFMQTEF 128

Qy 123 FLKSLTLEDVPHGKHVFCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENEVLV 182
Db 129 FLVSLTLEDIPNHGSIHFVCSWYNAKLKSDRIFFANQAYLPSETPAPLVKYRENEVLH 188

Qy 183 TLRGDGTCKLEWDRVYDYAYNDLGDGDPKQDLRSRVLGGSSEYPPRRGRTGRKPKTKT 242
Db 189 NLRGDTGERKEWERYDYDYNDLGDGDPKQDLRSRVLGGSSEYPPRRGRTGRKPKTK 248

Qy 243 DPNSESRIPLMSLDIYVPRDRFCHIKLSDFLTPALKSIVQLLLPEFKALFD--STHNE 300
Db 249 DPNSESR-----SNDVYLPRDEAFGLKSSDPLTYGLKSVSNVLPQLQSAFDLNFTRP 303

Qy 301 FDSPEVLKVEGGIKLPGQLLKAITSI-----PLEILKELLRSOGGLFKYPTPPQVIQ 356
Db 304 FDSFDEVHGLSYGGIKLP-----TDIISKISPLVPLKEIFRTDGEQALKFPPPKVIQ 355

Qy 357 EDKTAWRITDEEFGREMLAGVNPVILSRQEPKSLDPPKQDLRSRVLGGSSEYPPRRGRTGRKPKTK 416
Db 356 VSKSAWMTDEEPAREMLAGVNPVILSRQEPKSLDPPKQDLRSRVLGGSSEYPPRRGRTGRKPKTK 415

Qy 417 LTIDDAIKTNRLFIINLHDDIIMPYLRINTSDTKTYASRTILFLQDNGTLKPSAIELSL 476
Db 416 LTVDIAIQNKRLFLJLDDHDPIMPYLRIN-ATSTKAYATRIILFLKNGDLRPLAIELSL 474

Qy 477 PHPDGQGFAGSVKVTTPADQGVGSIWQAKAYAVNDSGVHQLISHNLTHAAIEPVI 536
Db 475 PHPDGQDQSGAFSQVLPADQGVGESSIWLLAKAYVYVNDSCYHQLVSHNLTHAVVEPFI 534

Qy 537 ATNRQLSALHPYIKLHPHFRETNNINARQILINGGLLELTVFPKAKYSMEMSAVVYK 596
Db 535 ATNRHLSVWHPYIKLHPHYRDTNINGLARLSLVNDGGVIEQTFLGRYSVENSAVVYK 594

Qy 597 DWVPEQALPTDLIKRGVAVEDSSPLGIRLLIODYPYAVDGLKIWSAISKSWTEYCNYY 656
Db 595 DWVFTDQALPADLTKRGMAIEDPSCPHGIRLVIEDYPYAVDGLIEIDAIAKTWVHEYVFLY 654

Qy 657 YKSDDAVQKDTLOAWMKELREEGHGDGKDEPPWPKMTQVQELIDSCITITWIASALHAA 716
Db 655 YKSDDTLREDPELQACWKELVEVGHGDKQNEPWWPKMTREELVEACAIIITWASALHAA 714

Qy 717 VNFQYYPAGYLPNRPILSRNFMPEPGSPSEYEEELKTNPKVFLKTIITPQLQTLGLISLIE 776
Db 715 VNFQYYPGGILNRPILSRNFMPEKGSAAVEELRKNPQKAYLKTITPKFQTLIDLVSIE 774

Qy 777 ILSRSHSDDTLYLQRESPEWTKDQEPISAFARFQKLSIDEDQIMQNVVDKWKNRSGPV 836
Db 775 ILSRSHASDEVYVLRDNPNTSDTRALEAFKRFNGKLAQIENKLSERNNDKLRNCGPV 834

Qy 837 KVPYTLPTSEGGLTGKIPNSVSI 862
Db 835 QMPYTLPLPSKGLTFRGIPNSISI 860

RESULT 9
US-10-425-114-54429
; Sequence 54429, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54429
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700842448_FLI.pep
US-10-425-114-54429

Query Match 64.2%; Score 2909; DB 15; Length 863;
Best Local Similarity 63.4%; Pred. No. 2.6e-228;
Matches 549; Conservative 122; Mismatches 159; Indels 36; Gaps 9;

Qy 16 GKVKGTWLMKKNVLDFT-----DINASVLDGVLEFLGRVSLLEISSVNA 62
Db 15 GHKIGTIVLMKKNVLDVNSVTSVGGIIGQGLDVGSTLDTLTAFLGRSVLSLQISATKA 74

Qy 63 DPANGLOKRSKAAAYLENLWNTSTPIAAGESAFRVTDFWDDDEEFGVGFATIKNLHFSEF 122
Db 75 D-ANG-KGKLGKATFLEGIITSLPTLGAGSAFKNFEMDDGS-GIPGAFYIKNFMQTEF 131

Qy 123 FLKSLTLEDVPHGKHVFCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENEVLV 182
Db 132 FLVSLTLEDIPNHGSIHFVCSWYNAKLKSDRIFFANQAYLPSETPAPLVKYRENEVLH 191

Qy 183 TLRGDGTCKLEWDRVYDYAYNDLGDGDPKQDLRSRVLGGSSEYPPRRGRTGRKPKTKT 242
Db 192 NLRGDTGERKEWERYDYDYNDLGDGDPKQDLRSRVLGGSSEYPPRRGRTGRKPKTK 251

Qy 243 DPNSESRIPLMSLDIYVPRDRFCHIKLSDFLTPALKSIVQLLLPEFKALFD--STHNE 300
Db 252 DPNSESR-----SNDVYLPRDEAFGLKSSDPLTYGLKSVSNVLPQLQSAFDLNFTRP 306


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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-17

Query Match      64.1%; Score 2905; DB 10; Length 857;
Best Local Similarity 63.3%; Pred. No. 5.5e-228;
Matches 548; Conservative 122; Mismatches 160; Indels 36; Gaps 9;

Qy 16 GKVKGTVLMKKNVLDFT-----DINASVLDGVLEFLGRVSLLEISSVNA 62
Db 9 GHKIGTIVLMKKNVLDVNSVTSVGGITGQGLDVLGSLDTLTAPLGRSVLSLISATKA 68

Qy 63 DPANGLOGKRSKAAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHSEF 122
Db 69 D-ANG-KGKLGKATFLEGIITSPLTGAGSAFKINFEDDGS-GIPGAFYIKNFMQTEF 125

Qy 123 FLKSLTLEDVPHGKHVFCNSWYVANKYSDRIFFANQAYLPSETDPTLRKYRENEVLV 182
Db 126 FLVSLTLEDIPNHGSIHFVNCNSWIYNAKLFKSDRIFFANQAYLPSETPAPLVKYREEELH 185

Qy 183 TLRGDTGKLEEDRWYVAYVNDLGDGDKGDLRSRVLGGSSEYPPRRGRTGKPKTK 242
Db 186 NLRGDTGERKEWERYDYVNDLGDGDKGENHARPVLGNDTPPYPRGRTGKPKTRK 245

Qy 243 DPNSESRIPLLMSLDIYPRDERFGHKLSDFLTPALKSIYQLLPEPKALFD--STHNE 300
Db 246 DPNSESR-----SNDVYLPRDEAFGLKSSDFLTGKSVSONVLPPLQSAFNLFTPRE 300

Qy 301 FDSPELVKLEGGIKLPQGLLKAITDSI-----PLEILKLLRSDDGGLFKYPTPQVIQ 356
Db 301 FDSFVHGLYSGGIKLP-----TDIISKISPLVKEIFRTDGEQALKFPPPKVIQ 352

Qy 357 EDKTAWRTDEEFGRLAGVNPVILSRLOEPPPKSLDPKLYGNQNSITIREQIEDKLDG 416
Db 353 VSKSAMWTEDEFAARMLAGVNPILRCLKDPFPRKLSQSVYGDHSTQITKEHLEPNLEG 412

Qy 417 LTIDEAIKTNRLFIILNHHDIIMPYLRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSL 476
Db 413 LTVDIAIQKRLFLDHDHPIMPYLRIN-ATSTKAYATRTILFKNDGTLRPLAIELSL 471

Qy 477 PHPDGQGFAGSVKVTTPADQGVESIWOLAKAYAAVNDSGVHOLISHWLNTHAAIEPVI 536
Db 472 PHPDGQDGSAGFQVLPADGVESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFI 531

Qy 537 ATNROLSALHPYKLLHPHFRETMINALARQILINGGLLELTVFPKYSMEASVYVK 596
Db 532 ATNRHLSVVHPYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTFWGRYSVEMSAYVK 591

Qy 597 DWVFPQEQALPDLIKRGVAVEDSSPLGIRLLIODYPYAVDGLKIWSAISKWVTEYCNVY 656
Db 592 DWVFTDQALPADLIRKGMALIEDPSCPHGIRLVIEDYPTVDGLEIWDALKTWVHEVFLY 651

Qy 657 YKSDDAVOKDTLOAWKLEBEHGDGKDEPNWPMQTVQELIDSCHITTIWIASALHAA 716
Db 652 YKSDTLREDPELQACWLEVEHGDGKKNPMPKMQTRBELVEACAIITWIASALHAA 711

Qy 717 VNFGQYPVAGYLPNRPITLSRNPMPGPGPEYBELKTNPKVFLKTTITPOLQTLIGISIE 776
Db 712 VNFGQYPVGLLILNRPITLSRNPMPKGAEBELRNPKQAYLTKITTFQTLIDLVSIE 771

Qy 777 ILSRHSSTLYLGQRESPEWTKDQPLSAFARFGKLSJDIEDQIQMNVDEKKNRSGPV 836
Db 772 ILSRHSASDEVYLGERNPNWTSDTTALAEAFKFGNKLQAIENKLSERNDEKLRNRCGPV 831

Qy 837 KVPYTLPTSEGGITGKIPNSVSI 862
Db 832 OMPYTLPLPSKKEGLTFRGIPIINSISI 857

RESULT 12
US-10-424-599-215973
; Sequence 215973, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215973
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37053C.1.pep
US-10-424-599-215973

Query Match      62.8%; Score 2849.5; DB 15; Length 826;
Best Local Similarity 62.7%; Pred. No. 1.8e-223;
Matches 535; Conservative 122; Mismatches 155; Indels 41; Gaps 9;

Qy 16 GKVKGTVLMKKNVLDFTDINASVLDGVLEFLGRVSLLEISSVNAADPANGLOGKRSKA 75
Db 9 GHKIGTIVLMKKNVLDVNSVTS--VGGII-----GQANG-RGKLGKA 48

Qy 76 AYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHSEFELKSLTLEDVPHN 135
Db 49 TFLGIIITSPLTGAGSAFKINFEDDGS-GIPGAFYIKNFMQTEFVLVSLTLEDIPNH 107

Qy 136 GKVFHVCNSWYVANKYSDRIFFANQAYLPSETDPTLRKYRENEVLVLRGDTGKLEEW 195
Db 108 GSIHFVNCNSWIYNAKLFKSDRIFFANQAYLPSETPAPLVKYREEELHNLRGDTGERKEW 167

Qy 196 DRVTDYAYNDLGDGDKGDLRSRVLGGSSEYPPRRGRTGKPKTKDTPNSESRIPLMS 255
Db 168 ERIYDYVNDLGDGDKGENHARPVLGNDTPPYPRGRTGKPKTRKDPNSES-----S 222

Qy 256 LDIVVPRDERFGHKLSDFLTPALKSIYQLLPEPKALFD--STHNEFDSPELVKLYEG 313
Db 223 NDVTLPRDEAFGLKSSDFLTGKSVSONVLPPLQSAFNLFTPREFDSFDEVHGLYSG 282

Qy 314 GIKLPQGLLKAITDSI-----PLEILKLLRSDDGGLFKYPTPQVIQEDKTAWRTDEEFG 369
Db 283 GIKLP-----TDIISKISPLVKEIFRTDGEQALKFPPPKVIQVSKSAMWTEDEFA 334

Qy 370 REMLAGVNPVILSRLOEPPPKSLDPKLYGNQNSITIREQIEDKLDGLTIDEAIKTNRLF 429
Db 335 REMLAGVNPVILRCLKEFPFPRKLSQSVYGDHSTQITKEHLEPNLEGTLVDEAIQNKELF 394

Qy 430 ILNHHDIIMPYLRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDGQDGFAGSVK 489
Db 395 LLDHDPIMPYLRIN-ATSTKAYATRTILFKNDGTLRPLAIELSLPHPDGQDGSAGFSQ 453

Qy 490 VYTPADQGVESIWOLAKAYAAVNDSGVHOLISHWLNTHAAIEPFIATNRQLSALHPYI 549
Db 454 VFLPADEGVESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFIATNRHLSVVHPYI 513

Qy 550 KLLHPHFRETMINALARQILINGGLLELTVFPKYSMEASVYVKDWMVPEQALPDL 609
Db 514 KLLHPHYRDTMNINGLARLSLVNDGGVIEQTFWGRYSVEMSAYVKDWMVTDQALPADL 573

Qy 610 IKRGVAVEDSSPLGIRLLIODYPYAVDGLKIWSAISKWVTEYCNVYKSDDAVOKDTL 669
Db 574 IKRGMAIEDPSCPHGIRLVIEDYPYAVDGLIEWDALKTWVHEVFLYKSDDTLREDEEL 633

Qy 670 QAWWKELEEGHGDGKDEPNWPMQTVQELIDSCHITTIWIASALHAAVNFQYPVAGYLP 729
Db 670 QAWWKELEEGHGDGKDEPNWPMQTVQELIDSCHITTIWIASALHAAVNFQYPVAGYLP 729
```

Db 634 QACWKELVEVGHDKKNEPWPQKQTRLEELVEACAIITWASALHAANVFGQVPGYGLL 693
Qy 730 NRPTLSRNFMPGSPGYEELKTNPKVFLKTTTPOQLTGLGSLIEILSRHSSDTLYLG 789
Db 694 NRPTLSRNFMPGSPGYEELKTNPKVFLKTTTPOQLTGLGSLIEILSRHSSDTLYLG 753
Qy 790 QRESPEWTKDQEPPLSAFARFGKGLSDIEDQIMQNVDEKWKNSRGPVKVPYTYLLFPTSEG 849
Db 754 ERDNPWTSITRALEAFKFGKGLAQIENKLSERNDEKLRNRCGVPQVMPYTYLLFPTSEG 813
Qy 850 GLTGKGINPSVSI 862
Db 814 GLTFRGIPNSISI 826

RESULT 13
US-10-425-114-45631
; Sequence 45631, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45631
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700733503_FLI.pap
US-10-425-114-45631

Query Match 62.8%; Score 2849.5; DB 15; Length 832;
Best Local Similarity 62.7%; Pred. No. 1.8e-223;
Matches 535; Conservative 122; Mismatches 155; Indels 41; Gaps 9;

Qy 16 GKXVGTVMKKNVLDFTDINASVLDGVLEFLGRVSVLELSSVNNADPANGLOGKRSKA 75.
Db 15 GHKIGTVMKKNVLDVNSVTS--VGGII-----GOANG-KGKLGKA 54
Qy 76 AYLENWLTNSTPIAAGESAFRTVDWDEFGVPGAFIINKLHFGSFFFLKSLTLEDVPH 135
Db 55 TLEGITSLPTLGAGQSAKINFEWDGSG-GIPGAFYIKNFMQTEFFLVSLTLEDIPNH 113
Qy 136 GKXVFCNSVWVPYANKYSDRIFFANQAYLPSETPTLKYRENELVTLRGDGTGKLEW 195
Db 114 GSIHFVCSWYNAKLKSDRIFFANQAYLPSETPTLKYRENELVTLRGDGTGKLEW 173
Qy 196 DRAVDYAYNDLGDQKODLSRPLVGSSEVYPRRGSTGRKPKYTDNSERSRPLMS 255
Db 174 ERIYDYVDVNDLGDQKODLSRPLVGSSEVYPRRGSTGRKPKYTDNSERSRPLMS 228
Qy 256 LDYVPRDRFCHIKLSDFLTALKSIVQLLPKALFD--STNEPFSFDVLKLYEG 313
Db 229 NDVYLPRDEAFHKLSSDLTGLKSVSNVPLQSAFDLNTFPREFDSFVEVGLVSG 288
Qy 314 GIKLPQGLLKAITDSI-----PLEIKELLRSDBGLFKYPTPOVQIEDKTAWRTDEEFG 369
Db 289 GIKLP-----TDIISKISPLVLEIFRTDGEQALKFPKPKVQVQSKSAMWTDDEEFA 340
Qy 370 REMLAGVNPVILSRQEPKPKSLDPKPKYGNQNSITREQIEDKLDGLTIDAIKTNRLF 429
Db 341 REMLAGVNPVILSRQEPKPKSLDPKPKYGNQNSITREQIEDKLDGLTIDAIKTNRLF 400
Qy 430 ILNHHDILMPLYLRINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHPDGDQFGAVSK 489

Db 401 LLDHEDPMPYLRRIN-ATSTKAYATRIILFLKNDGTLRPLAIELSLPHPDGDQSGAFSQ 459
Qy 490 VYTPADQGVGEGSIWQIAKAYAAVNDGSGVHQLISHMLNTHAAIEPFIATNRQLSAHPYIY 549
Db 460 VFLPADEGVGESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFIATNRHLSVVHPYIY 519
Qy 550 KLLHPHFRETWNINALARQILLINGGLLELTVFPKYSMEMSAVVYKDWVFPQALPTDL 609
Db 520 KLLHPHYRDTMNINGLARLSLVNDGVTQTLWGRYSVEMSAVVYKDWVFPQALPTDL 579
Qy 610 IKRGVAVEDSSPLGIRLLIOPYAVDGLKTIWSAKSWVTYCNYYKSDDAVQKDTL 669
Db 580 IKRGMAIEDPSPGHGIRLVIEDPYAVDGLKTIWSAKSWVTYCNYYKSDDAVQKDTL 639
Qy 670 QAWKELREEGHDKKDEPWPQKQTRLEELVEACAIITWASALHAANVFGQVPGYGLL 729
Db 640 QACWKELVEVGHDKKNEPWPQKQTRLEELVEACAIITWASALHAANVFGQVPGYGLL 699
Qy 730 NRPTLSRNFMPGSPGYEELKTNPKVFLKTTTPOQLTGLGSLIEILSRHSSDTLYLG 789
Db 700 NRPTLSRNFMPGSPGYEELKTNPKVFLKTTTPOQLTGLGSLIEILSRHSSDTLYLG 759
Qy 790 QRESPEWTKDQEPPLSAFARFGKGLSDIEDQIMQNVDEKWKNSRGPVKVPYTYLLFPTSEG 849
Db 760 ERDNPWTSITRALEAFKFGKGLAQIENKLSERNDEKLRNRCGVPQVMPYTYLLFPTSEG 819
Qy 850 GLTGKGINPSVSI 862
Db 820 GLTFRGIPNSISI 832

RESULT 14
US-10-437-963-165232
; Sequence 165232, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165232
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64058C.1.pap
US-10-437-963-165232

Query Match 61.6%; Score 2791.5; DB 16; Length 888;
Best Local Similarity 61.2%; Pred. No. 1.1e-218;
Matches 534; Conservative 120; Mismatches 198; Indels 21; Gaps 8;

Qy 8 DAITGKD-----DGKKVGTVMKKNVLDFTDINASVLDGVLEFLGR--VSLELISSV 60
Db 19 DRLTGRNKEAWKEG-RIRGTAVLVKKDVLGLDFHSLLDGVHNLHGKEGVAFRLVSAT 77
Qy 61 NADPANGLOGKRSKAAVLENWLTNSTPIAAGESAFRTVDWDEFGVPGAFIINKLHFS 120
Db 78 ARDPSNGRGKLGKPAHLEELVVTWMTAAGESVFRVAFWDESO-GIPGAVVVTNSNR 136
Qy 121 EFFKSLTLEDVPHNKGKVFHFCNSVWVPYANKYSDRIFFANQAYLPSETPTLKYRENE 180

Db 137 EFFLKTLLDGVGPGKGTGVVANSWIPADNYQYERVFANDTYLPSSQWPAFLPYRQEE 196
Qy 181 LVTLEDCG-TGKLEWDRVYAYYNDLGDPPKQDLSRPVLGSGSEYPPRRGRTGRKP 239
Db 197 LNLFGDKIGPYKEHDIYRYDYNDLQDPQKSLVRPVLGGSELPYRRGRTGRAP 256
Qy 240 TKTDNSRSRPLMLSLDIYVPRDERFGHKLSDFLTFALKSIQVLLPPEFKALFDSHTN 299
Db 257 TKTDNTRSRLPL-DLNIYVPRDERFGLKMSDFLKSIAIEGVLPILRTIYVDTTPK 315
Qy 300 EFDSEFVLYEGGKILPOGPELLKAITSDISPLEILKELLRSDEGLFKYPTQVIOEDK 359
Db 316 EFDSPDIMELEYEGGLKVANASALAEIKRVPFELIKSLPVAGQVQLPLPHVikedK 375
Qy 360 TAWRTDEFEGBMLAGVNPVLSRLOEPFKSLDKPKIYGNQNSTITREQIEDKLDGLTI 419
Db 376 FAWRTDEEFAREMLAGVNPVIMKRLTNFPKSLDLPNVYGDHTSKITAEHAKHNEGTLV 435
Qy 420 DEAIKTNRLFILNHDHILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPH 479
Db 436 QVALKGNRLFILNHDHILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPH 495
Qy 480 DQDQFAGVSKVYTPADQGVESQIWOLAKAYAVNDSGVHQLISHWLNTHAAIEPEVIATN 539
Db 496 DQDQFAGVSKVYTPANTGVESQIWOLAKAYAVNDSGVHQLISHWLNTHAAIEPEVIATN 555
Qy 540 ROLSALHPIYKLLHPHRETMINALAQIILINGGGLLELTVFPKAYSMEMSAVYKDW 599
Db 556 ROLSALHPIYKLLHPHRETMINALAQIILINGGGLLELTVFPKAYSMEMSAVYKDW 615
Qy 600 FPEQALPTDLIKRGVAVDSPLGIRLLIODYPVAVDGLKIWSAISKWVTEYCNYYKS 659
Db 616 FTEQALPVDLKRGVAVDPSTSPYVNRLLIKDYPVAVDGLKIWSAISKWVTEYCNYYKS 675
Qy 660 DDAVQKTELQAWKELREEGHDKKDPFMPKMTQVQELIDSCITTIWIASALHAAVNF 719
Db 676 DGVLRGDEELQAWKELREEGHDKKDPFMPKMTQVQELIDSCITTIWIASALHAAVNF 735
Qy 720 GOYPYAGVLPNRPVLSRNPMPPEGSPEEELKTNPKD---VFLKTIITPOLQTLGILIE 776
Db 736 GOYPYAGVLPNRPVLSRNPMPPEGSPEEELKTNPKD---VFLKTIITPOLQTLGILIE 795
Qy 777 ILSRHSSTLYLGQRESPEWTKDQPLSAFARFGKLSIDEDQIMQMVNDKWKNSGPV 836
Db 796 ILSKSSDEVILGQDTPETWSDAKALDAFRFGSLVDIENRIKDMNGNSALKWNGPV 855
Qy 837 KVPYTLFPPTSEG-----GLTGKIPNSVSI 862
Db 856 KMPYMLLYPNTSDVTKEKGQGLTAMGIPNSISI 888

RESULT 15
US-10-424-599-220216
; Sequence 220216, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 220216
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(860)

; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40885C.1.pap
US-10-424-599-220216

Query Match 61.5%; Score 2790; DB 15; Length 860;
Best Local Similarity 60.9%; Pred. No. 1.4e-218;
Matches 525; Conservative 129; Mismatches 178; Indels 30; Gaps 7;
Qy 17 KVVGTGTVLMKKNVLDFTDINA-----SVLDGVLEFLGRVSLSELISVSNAD 63
Db 13 QKVGTVLMKKNVLDINSITSVRGLICTGINIIGSTIDGLTSFLGRSVCLQISATKAD 72
Qy 64 -PANGLOGKSKAAYLENWLTNSTPIAGSAPVTFDWDDEERGVCAPFIIKNLHPEF 122
Db 73 GNGVGVGKKT---YLEGIIITSITLGGAGSAFTIHFEW--DADMGIPGAFILKNMQVEL 128
Qy 123 FLKSLTLEDVPHGKVFVCNSWYYPANKYKSDRIFFANQAYLPSETPTDLTKRYENELV 182
Db 129 FLVSLTLEDIPNQGSMHFVCNSWYNSKVYEKDAIFPASETYVPSETPGPLVTRYAEALQ 188
Qy 183 TLRGDTGKLEWDRVYAYYNDLGDPPKQDLSRPVLGSGSEYPPRRGRTGRKPKTK 242
Db 189 ALRGNGTKRKEWDRVYDYNDLGNPDSGENFARPVLGSLTHPYPRGRTGRKPKTK 248
Qy 243 DPNSERIPMLSLDIYVPRDERFGHKLSDFLTFALKSIQVLLPPEFKALFD--STHNE 300
Db 249 DPNSEK-----PGEAYIPRDENFGHLKSSDFLYGKLSRSLFPAUKTVDFINFTPNE 302
Qy 301 FDSFEDVLYEGGKILPOGPELLKAITSDISPLEILKELLRSDEGLFKYPTQVIOEDKT 360
Db 303 FDSFEEVRLCEGKILPTDILSKI-----SPLVLEIFRTDGSVLKFSVPDLIKVSKS 358
Qy 361 AWRDSEFGREMLAGVNPVLSRLOEPFKSLDKPKIYGNQNSTITREQIEDKLDGLTID 420
Db 359 AWMDESFAREMIAGVNPVIRLQEPFPQKLPDSVYQDTSKMTIDHLEINLEGLTVD 418
Qy 421 EAIKTNRLFILNHDHILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHD 480
Db 419 KAIQKQRLFILNHDHILMPYLRRINTSDTKTYASRTLLFLQDNGTLKPSAIELSLPHD 478
Qy 481 GDQFAGVSKVYTPADQGVESQIWOLAKAYAVNDSGVHQLISHWLNTHAAIEPEVIATNR 540
Db 479 QQQLGAYSKVILPANQGVESQIWOLAKAYAVNDSGVHQLISHWLNTHAAIEPEVIATNR 538
Qy 541 QLSALHPIYKLLHPHRETMINALAQIILINGGGLLELTVFPKAYSMEMSAVYKDWVF 600
Db 539 NLSILHPIYKLLHPHRETMINALAQIILINGGGLLELTVFPKAYSMEMSAVYKDWVF 598
Qy 601 PEQALPTDLIKRGVAVDSPLGIRLLIODYPVAVDGLKIWSAISKWVTEYCNYYKSD 660
Db 599 LDQALPADLIRKGNWAIEDSCPNGLRLVIEDYPVAVDGLKIWSAISKWVTEYCNYYKSD 658
Qy 661 DAVOKTELQAWKELREEGHDKKDPFMPKMTQVQELIDSCITTIWIASALHAAVNF 720
Db 659 DAIKKDELQAWKELREEGHDKKDPFMPKMTQVQELIDSCITTIWIASALHAAVNF 718
Qy 721 QYPYAGVLPNRPVLSRNPMPPEGSPEEELKTNPKD---VFLKTIITPOLQTLGILIEILSR 780
Db 719 QYPYAGVLPNRPVLSRNPMPPEGSPEEELKTNPKD---VFLKTIITPOLQTLGILIEILSR 778
Qy 781 HSDTLYLGQRESPEWTKDQPLSAFARFGKLSIDEDQIMQMVNDKWKNSGPV 840
Db 779 HASDEVILGQDTPETWSDAKALDAFRFGSLVDIENRIKDMNGNSALKWNGPV 838
Qy 841 TLLFPPTSEGGLTGKIPNSVSI 862
Db 839 TVLLPPTSEGGLTGKIPNSVSI 860

Search completed: March 10, 2005, 19:06:19
Job time : 154 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 13, 2005, 22:52:34 ; Search time 1087 Seconds
(without alignments)
4694.404 Million cell updates/sec

Title: US-10-731-642A-1

Perfect score: 4534

Sequence: 1 MFLEKIVDAITGDKGKKV.....LPTSEGGLTGKIPNSVSI 862

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPRO_spool/US10731642/runat_10032005_102235_5450/app_query.fasta_1.1031
-DB=N Geneseq_16Dec04 -QPMF=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10731642 -CGN_1_547 @runat_10032005_102235_5450 -NCPUS=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4534	100.0	3390	8	ABZ68210 Nucleotid
2	3620.5	79.9	2871	2	AAT60428 Tomato fr
3	3463.5	76.4	2441	2	AAT60429 Tomato fr
4	3254.5	71.8	4237	9	ACD28852 Wine grap
5	3202.5	70.6	2580	6	ABZ13699 Arabidops

6	3202.5	70.6	2580	8	ADA67958	Arabidops
7	3138	69.2	4687	9	ACD28851	Wine Grap
8	3054	67.4	2562	8	ABX13452	A. thalia
9	3022.5	66.7	2929	9	AA157712	Balsam pe
10	2911	64.2	2964	4	AAF88022	Cucumber
11	2911	64.2	2964	8	ABX13453	C. sativu
12	2779.5	61.3	2595	10	AAD64729	Maize lip
13	2779.5	61.3	3007	10	AAD64728	Maize lip
14	2769.5	61.1	2595	10	ADG93380	Maize lip
15	2769.5	61.1	3007	10	ADG93378	Maize lip
16	2734.5	60.3	2664	10	ADG93388	Maize lip
17	2734.5	60.3	3080	10	ADG93386	Maize lip
18	2724.5	60.1	2664	10	ADG93396	Maize lip
19	2724.5	60.1	2664	10	ADG93392	Maize lip
20	2724.5	60.1	3122	10	ADG93390	Maize lip
21	2724.5	60.1	3134	9	AA157714	Corn (Zea
22	2700.5	59.6	2622	10	ADG93372	Maize lip
23	2700.5	59.6	2912	10	ADG93370	Maize lip
24	2694.5	59.4	2613	8	ADA69728	Rice gene
25	2682	59.2	3033	10	ADC53127	'-specif
26	2680	59.1	2818	6	ABK88441	Barley li
27	2680	59.1	2818	6	ABK88515	DNA encod
28	2634.5	58.5	2559	8	ADA70433	Rice gene
29	2605	57.5	2516	9	ADA48505	Rice gene
30	2585.5	57.0	2616	10	ADG93384	Maize lip
31	2585.5	57.0	2949	10	ADG93382	Maize lip
32	2563	56.5	2830	2	AAQ24492	Rice lip
33	2563	56.5	2830	2	AAQ24234	Lipoxigen
34	2404.5	53.0	2566	12	ADJ39813	Plant CDN
35	2386	52.6	2115	8	ADA69794	Rice gene
36	2329.5	51.4	7059	2	AAQ44750	Soybean l
37	2280.5	50.3	4663	6	ABK88440	Barley li
38	2280.5	50.3	4663	6	ABK88514	Wild type
39	2280.5	50.3	4663	6	ABK88522	DNA encod
40	2273.5	50.1	4663	6	ABK88445	Barley li
41	2273.5	50.1	4663	6	ABK88442	Barley li
42	2273.5	50.1	4663	6	ABK88521	DNA encod
43	2273.5	50.1	4663	6	ABK88516	DNA encod
44	2259	49.8	4483	10	ADG93425	Maize lip
45	2259	49.8	7492	10	ADG93422	Maize lip

ALIGNMENTS

RESULT 1
ABZ68210
ID ABZ68210 standard; DNA; 3390 BP.

XX AC ABZ68210;

XX DT 07-APR-2003 (first entry)

XX DE Nucleotide sequence comprising CaMV 35S promoter and tobacco Lox1.

XX KW Lipoxigenase-1; LOX-1; enzyme; plant; dioxygenation;

XX KW polyunsaturated fatty acid; pentadiene; disease resistance; Solanacea;

XX KW tobacco; tomato; potato; pepper; gene; ss.

XX OS Nicotiana tabacum.

XX FH Key Location/Qualifiers

XX FT promoter 1..532

XX FT CDS /tag= a

XX FT /note= "CaMV 35S promoter"

XX FT /tag= b

XX FT /product= "LOX1"

XX FT /note= "6"

XX FT terminator 3138..3390

XX FT /tag= c

XX FT /note= "Nos terminator"

PN W0200299112-A2.

QY 521 IleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArg 540
 Db 2103 ATCAGTCACTGGTTGAATACACATGCGAGGATAGAGCCATTGCGATCGCAACAATAGG 2162
 QY 541 GlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMet 560
 Db 2163 CAACTAAGCGCGCTTACCCCTATTATTAAGCTTCTCCACCCTCATTTCCGTGAGACGATG 2222
 QY 561 AsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThr 580
 Db 2223 AACATATAGCTTTAGCAGACAGATCTTGATCAACGGTGGGAGCTTCTTGAGTTGACA 2282
 QY 581 ValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhe 600
 Db 2283 GTTTTTCGGCCCAATATTCCATGGAATGTGAGCAGTAGTTTACAAAGACTGGGTTTC 2342
 QY 601 ProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSer 620
 Db 2343 CCGTAACACAGCACTTCTACTGATCTCATCAAAAGAGGAGTAGCTGTTGAGGACTCGAGC 2402
 QY 621 SerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAlaAspGlyLeuLys 640
 Db 2403 TCCCCACTGGCATTCGATTACTGATTCAGGACTATCCATATGCTGTGATGGGTTGAAA 2462
 QY 641 IleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAsp 660
 Db 2463 ATTTCGTGAGCAATTTAAAGTTGGGTAACTGATGATCACTCACTACTATTACAATCAGAT 2522
 QY 661 AspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGly 680
 Db 2523 GATCGGTTTCAAAAGACACTGAACTCCAAAGCTGGTGAAGGAACTCCGCGAAGAGGA 2582
 QY 681 HisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIle 700
 Db 2583 CACGTGACAAAGAGATGAGCTTGGTGGCTTAAATGACACAGCTGCAAGAAATGTATA 2642
 QY 701 AspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGly 720
 Db 2643 GACTCTGCACCATCACAATATGATAGCTTCCAGCACTTCATGAGCAGTCAATTTGGG 2702
 QY 721 GlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetPro 740
 Db 2703 CAATACCCCTATGCTGGTTATCTCCCTAATCGCCCTACATTAAGCGCAAAATTTATGCCA 2762
 QY 741 GluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLys 760
 Db 2763 GAGCCGGAAGTCCGTGAGTATGAAGAGCTCAAGACAAATCCGGATAGGTATTCCTCAA 2822
 QY 761 ThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArg 780
 Db 2823 ACAATCACTCTCAGTCGAGACACTGCTGGCATTTCCCTCATAGAGATCTTGTCAAGG 2882
 QY 781 HisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGln 800
 Db 2883 CATTCCTCGGATACACTTTACCTCGGCAAGAGGAATCACCTGAATGCAAAAGGATCAA 2942
 QY 801 GluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIle 820
 Db 2943 GAACACATTTTCAGCTTTTCGCGAGGTTTGGAAAGAGCTGAGTGATATCGAGGATCAGATT 3002
 QY 821 MetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyr 840
 Db 3003 ATGCAGATGAATGTCGATGAGAAATGGGAAGACAGCTCGGTCCTGTAAAGTTCCATAC 3062
 QY 841 ThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerVal 860
 Db 3063 ACCTTGCTCTTCCCCACAAGTGAAGAGGAGCTTATCGGCAAGGAATTCCTAACAGTGTG 3122
 QY 861 SerIle 862
 Db 3123 TCAATA 3128
 RESULT 2

AAT60428
 ID AAT60428 standard; cDNA; 2871 BP.
 XX
 AC AAT60428;
 XX 27-AUG-2003 (revised)
 DT 08-JUL-1997 (first entry)
 XX Tomato fruit ripening specific lipoxygenase gene.
 XX LOX gene; fruit ripening specific lipoxygenase; FRS-LOX; tomato;
 KW transgenic plant; ss.
 XX Lycopersicon esculentum.
 FH Key Location/Qualifiers
 primer_bind 281..297
 FT /*tag= a
 FT /note= "primer used to amplify a FRS-LOX gene fragment
 FT (nucleotides 1-297)"
 XX
 XX WO9713851-A1.
 PN 17-APR-1997.
 XX 11-OCT-1996; 96WO-US016387.
 PF 13-OCT-1995; 95US-0005404P.
 PR (PURD) PURDUE RES FOUND.
 PA Handa AK, Kausch KD;
 XX WPI; 1997-235887/21.
 DR
 XX New transgenic plants with fruits having improved quality - obtained by
 PT transforming plant cells so as to inhibit production of fruit ripening
 PT specific lipoxygenase in fruits.
 XX Claim 5; Fig 4; 38pp; English.
 CC A tomato fruit ripening specific lipoxygenase (FRS-LOX) gene cDNA clone
 CC (AAT60428) was isolated from a red-ripe pericarp library using antibodies
 CC raised against a 90 kDa protein that accumulates in ripe fruit. The cDNA,
 CC or fragments of it (see also AAT60429-30), can be incorporated, in sense
 CC or antisense orientation, into vectors under control of e.g. the CaMV 35S
 CC promoter. The vectors are used to create transgenic fruit-bearing plants,
 CC esp. tomato, in which native FRS-LOX gene expression is inhibited. These
 CC plants can provide fruits having superior characteristics such as
 CC improved quality and texture, greater firmness, longer shelf life, better
 CC packaging and storage characteristics and improved processing
 CC characteristics. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 2871 BP; 888 A; 545 C; 614 G; 824 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 2871
 Score: 3620.50 Matches: 684
 Percent Similarity: 87.37% Conservative: 70
 Best Local Similarity: 79.26% Mismatches: 104
 Query Match: 79.85% Indels: 5
 DB: 2 Gaps: 3

US-10-731-642A-1 (1-862) x AAT60428 (1-2871)

QY 1 MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysLysValLys 20
 Db 45 ATGCTTTGGTGGGAATTGTGATGCCATCTTGGAAAGATGATAGCCAAAGTGAAA 104
 QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40
 Db 105 GGAAGAGTGATTTTGTGATGAAAAAAATGTTCTAGACTTCATTATATAGTGTCTTCA 164

QY 41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuLeuSer---Ser 59
DB 155 GTTGATGCAATTTCTGATTTCTTGGCCAAAGGCTCTATCCAAATGATAGTGGTTCT 224
QY 60 ValAsnAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGlu 79
DB 225 GTTAATTATGAT-----GGTTGGAAGGAACTGAGCAATCCAGCATACTTAGAG 275
QY 80 AsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99
DB 276 AGTTGGCTTACAGACATCAACCCCAATAACAGCAGGGGAATCAACTTTTAGTGTATACATTT 335
QY 100 AspTrpAspGluPheGlyValProGlyAlaPheIleLeuLysAsnLeuHisPhe 119
DB 336 GACTGGGATCGTACGAGTTGGAGTTCGAGGAGCATTCATCATCAAGAACTTCATCTT 395
QY 120 SerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHis 139
DB 396 AATGAGTTCTTTCTCAAGTCACTCACCTCGAAGATGTTCTTAATTATGGAAATATCCAT 455
QY 140 PheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePhe 159
DB 456 TTTGTATGCAATTTCTTGGGTTATCTCTGCTTTTAGATACAAGTCTGACCGCATTTTCTTT 515
QY 160 AlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuAtgLysTyrArgGluAsn 179
DB 516 GCCAATCAGGCTTATCTCCCAAGTGAACACCAACCATTTGCGNAATACAGAGAAAT 575
QY 180 GluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTyrAspArgValTyr 199
DB 576 GAACCTGGTAGCTTTCGAGGAGATGGAATCGAAGCTTGAAGATGGAGCGGTTTAT 635
QY 200 AspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgPro 219
DB 636 GATTATGCTTGTCTACAAATGACTTGGGTGAACCCAGATAAGGGGGAAGATATGCTAGGCCT 695
QY 220 ValLeuGlyGlySerSerGluTyrProTyrProArgAlaGlyArgTyrGlyArgLysPro 239
DB 696 ATCTTGGAGGTCCTCTGAGTACCCGTATCTCTGATAGGAGGAGCAGGCGCGAACA 755
QY 240 ThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyr 259
DB 756 ACCAAAGCAGATCCTAAATTCGAGAGCAGGAACCCATTTGCCTATGAGCTTAGACATATAT 815
QY 260 ValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeu 279
DB 816 GTCCCAAGGGAGCAGCGAATTTGGTCATGTGAAGAAAGTCAGACTTTTTCACGTCGTCCTTA 875
QY 280 LysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsn 299
DB 876 AAATCTCTTTCGCAACGCTTCTCCTCGGTTTAAGGCTTTGTGCGATAACACGCTAAT 935
QY 300 GluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuProGln 319
DB 936 GAGTTCAATAGCTTTGGCGATGTACTTAATCTCTATGAAGGAGGAATCAAGTTGCTGAA 995
QY 320 GlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeu 339
DB 996 GCGCCCTTGGTTGAAGCCATTACTGATACATATTTCCCTCAGAGATATAAAGACATCTCT 1055
QY 340 ArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLys 359
DB 1056 CAAACGGATGTCAGGCTTACTTAAGTACCCCACTCTCTCAGTTATTTCAGGCGATAAA 1115
QY 360 ThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProVal 379
DB 1116 ACTGCATGAGGAGCGGATCAAGAAATTTGGAGAGAAATGTTGGCAGGATCCAATCCTGTC 1175
QY 380 IleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGly 399
DB 1176 TTAATCAGTAGACTCCAAAGAAATTTCTCCGAAAGAGCAAGTTGGATCCCAACCATATATGA 1235
QY 400 AsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIle 419

DB 1236 AACCAAAACAGTACAATTCACAGAACATCTACAGGTAAGTTGAATGGATTAAACAGTG 1295
QY 420 AspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetPro 439
DB 1296 AATGAGGCAATCAAGAGTAACAGGTTATTCATATTGAACACCATGACATCGTATGCCA 1355
QY 440 TyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeu 459
DB 1356 CTATTGGAGAAATTAACATGTTCAGCAAAACACAAAAGCCTATGCTCAAGAACTCTGCTC 1415
QY 460 PheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisPro 479
DB 1416 TTCTTACAGATGATAGACTTTGAAGCCACTAGCAATTTGAATTAAGCTTCCACATCCA 1475
QY 480 AspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGlu 499
DB 1476 GACGAGATCAATTTGGTACTGTTAGTAAAGTATATACACAGCTGACCAAGGTGTTGAA 1535
QY 500 GlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGln 519
DB 1536 GGTTCTATCTGGCAGTTTGCCAAAGCCTATGTAGCAGTGAATGACATGGGCATTCATCAG 1595
QY 520 LeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsn 539
DB 1596 CTCAATTAGCCACTGGTTGAATACACACGCGTGATCGAACCATTTGTGATTGCAACAAT 1655
QY 540 ArgGlnIleSerAlaLeuHisProIleTyrLysLeuHisProHisPheArgGluThr 559
DB 1656 AGGCATCTAAGTGTGCTTCATCCCATTCATAAACTTCTTCATCTCTCATTTCCGTAACACG 1715
QY 560 MetAsnIleAsnAlaLeuAlaAspGlnIleLeuIleAsnGlyGlyLeuLeuGluLeu 579
DB 1716 ATGAACATAAATGCTTTAGCAAGAGAGACCTTTGACCTATGATGGTGGT---TTTGAGACG 1772
QY 580 ThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpVal 599
DB 1773 TCTCTTTTCTCCCAATATTCATGGAATGTCAGCAGCAGCTTACAAAGATTGGGTT 1832
QY 600 PheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSer 619
DB 1833 TTCCCTGAACAGCACTTCTCTGCTGATCTCTCAAAAGAGGAGTGGCTGTGTGAGGACTTG 1892
QY 620 SerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeu 639
DB 1893 AGCTCCCAACATGCGATTCGTTTACTGATCTGACTATCCATATGCTGTGTGATGGCTTG 1952
QY 640 LysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSer 659
DB 1953 GAAATTTGGGCGAGCAATCAAAAGTTGGTAAACAGATATTTCAGAGTTCTATTACAAATCT 2012
QY 660 AspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGlu 679
DB 2013 GACGACAGTAGAGAAAGACACTGAACTCCAAAGCTGGTGGAAAGGAGCTCCGCGAAGAA 2072
QY 680 GlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeu 699
DB 2073 GGACATGCGCAAGAAAGATGAGGCTTGGTGGCTTAACCTGCAAACTCGCAAGAGCTC 2132
QY 700 IleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPhe 719
DB 2133 AGAGATTGTTGCACCATCATTTATATGATAGTCTTCAGCACCTTCATGACGACTCCATTTT 2192
QY 720 GlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMet 739
DB 2193 GGCTTATACTCTTACGCTGGTTATCTCCCTAATCGCCCTACTTTAAGCTGTAATTTGATG 2252
QY 740 ProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeu 759
DB 2253 CCAGAGCCAGGAAGTTGAGTATGAGAGCTCAAGACAAATCCAGACCAAGGATATCTCTA 2312
QY 760 LysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluLeuLeuSer 779

383 ----- 383
1740 TACAGCTTCCTTTCAAATATTTTAAATGCCCTGTTGTTTCTGAGAAATGGAACCTTG 1799
383 ----- 383
1800 GAAAGGCTTCAGAGCTTTGTTTCTTCCCTCCATCTACTGTTCTAGCTCTTTTCTGATA 1859
384 -----
1860 ATTATGCTTTTCTTCTACTTTGTTGAGGAGTTTCTCCAAAAGCAAGCTGATCCTG 1919
396 ysileTyGlyAsnGlnAenSerThrileThrArgGluGlnileGluAspLysLeuAspG 416
1920 AAGTTTATGGCAACCAAAACAGTTCAATACCAAGAACACATAGAGAACTCACCTGGATG 1979
416 lyLeuThrIleAspGluAla ----- 422
1980 ACCTTACTATAAACGAGGT-AACGCTCTTAGGTTCCCTTCTTTCAGACTAAATTTTCAA 2038
422 ----- 422
2039 TGTCGACATGTAATTTTTTTCGATCGGAACCAAGCCATAGTAAGTGAATAATGCTGCTT 2098
423 ----- IleLysThrAsnArgLeuPheIleLeuAsnHisAspileLeuMetp 439
2099 TTTACTAGCAATGGAGAGAGAGGCTATTATATATAGATCACATGATGTTTTCATGC 2158
439 roTyLeuArgArgileAsnThrSerThrAspThrLysThrTyAlaSerArgThrLeuL 459
2159 CATACCTCAGGAGGATAAACACA---ACTTCCAGGAAACTATGCTCCCTCAAGGACTCTCC 2215
459 euPheLeuGlnAspAsnGlyThrLeuLysProSerAlaileGluLeuSerLeuProHisP 479
2216 TCTTCTGAAAGACGACGGAACCTTTTGAAGCCACTGGCGATTAATGAGCTTACCACATC 2275
479 roAspGlyAspGlnPheGlyAlaValSerLysValTyThrProAlaAspGlnGlyValG 499
2276 CTAGTGGGATTAATTTGGAGCTGTCAACAAGATATATACCCAGCTGAAATGTTGTTG 2335
499 luGlySerileTyPdpGlnLeuAlaLysAlaTyAlaAlaValAsnAspSerGlyValHisG 519
2336 AAGGTTCCATTTGGCAGCTGGCTAAAGCTTATGCTGCTGTGAATGACTCTGGCTATCATC 2395
519 lnLeuLeuSerHisTrpLeu ----- 525
2396 AGCTCTCAGCCACTGGTA-TGTAATATCCCAAGGAAAGTGAATACAGTTTGGGCTTAA 2454
526 ----- AsnThrHisAlaAlaI 531
2455 ATCTGAACGGGTGTGAATATCTTTGATGTTGTTGAGGTTGATACATGCTGCA 2514
531 leGluProPheValileAlaThrAsnArgGlnLeuSerAlaLeuHisProileTyLysL 551
2515 TTGAGCCATTTGTGATTCACCAACACGAGCTCAGCGTCTCATCAATTCACAGC 2574
551 euLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuI 571
2575 TTTTGCATCCTCCTCCGTGATCAATGAATGAATGAATGAATGAATGAATGAATGAATGA 2634
571 leAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLysTySerMetGluMetS 591
2635 TCATGCTGGTGGAGTGGAGACAGATTTTTCATCAAGTATGCCATGGAATGT 2694
591 erAlaValValTyLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuileL 611
2695 CATCTGTTGTTTACAAAGACTGGGTTCTTACTGAGCAAGCACTTCTCTGCTGATCTCATCA 2754
611 ys ----- 611
2755 A-GAGGTATATAAATCTGTTAGTGAATGTTTCTTCTTCTGCTGGAATGAATCTAGTG 2813
612 -----ArgGlyVala 615

Db 2814 AAAATTGTGATTTTCATTAATCTATGCTGCAACTTGGCACTCTTTCAGAGGAATGG 2873
Qy 615 laValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyProTyra 635
2874 CGGTTGAGGATTCAGAGGCTCTCATGGACTCCGCTACTGATAGTACTACCCCTATG 2933
Qy 635 laValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyCysAsnT 655
2934 CTGTTGATGGAATTCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2993
Qy 655 yrTyTyLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysG 675
2994 TCTACTACAGACAGATGAGTGTCCAGAAAGACTCTGAGCTTCAGTCTGTTGGGAAG 3053
675 luLeuArgGluGluGlyHisGlyAspLysAspGluProTyTrpProLysMetGlnT 695
3054 AAGTCAGGAAGAGGCTCATGGCACAAGAGGACGAGCCCTGGTGGCTAAAATGCATA 3113
Qy 695 hrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisA 715
3114 CTGTCAAAGAGCTGATAGAAACATGCACCATATCATCTGGGTGGCTTCTGCTCTCCATG 3173
Qy 715 laAlaValAsnPheGlyGlnTyProTyAlaGlyTyLeuProAsnArgProThrLeuS 735
3174 CTGAGTGAAATTCGGGAGTACCTCTTATGAGGCTACTCCCAACCGCCCAAGATAA 3233
735 erArgAsnPheMetProGluProGlySerProGluTyGluGluLeuLysThrAsnProA 755
3234 GCCGAGATTCATGCTGGAAGAGGCACTCTGAGTATGAAGAACTCAAGTCCAATCCTG 3293
Qy 755 spLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuI 775
3294 ATAAGGCTTCTCTGAAACCAATCATCTGCCAGCTGCAGACCTTCTTGGCATCTCCCTTA 3353
Qy 775 leGluIleLeuSerArgHisSerSerAspThrLeuTyLeuGlyGlnArgGluSerProG 795
3354 TTGAGGCTCTTCCAGGATCTTCCGATGAGGTTTATCTTGGACAGAGACACTCTCTG 3413
795 luTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerA 815
3414 AATGGACCTCGACACACACCACTTGAAGCTTTTGAAGAAATTCGGAAGGAGCTGGCAG 3473
Qy 815 spIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyP 835
3474 ACATTTGAAGAAATCATGATAGAAATGGAATGAGAGATTCAGAAACAGAGTTTGGC 3533
Qy 835 roValLysValProTyThrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysG 855
3534 CTGTGAAGATACCATACACTGCTCTACCCCAACAGGAGGTTGGCTTACTGGCAAG 3593
Qy 855 lyIleProAsnSerValSerIle 862
3594 GGATTCCAACAGGTCTCCATC 3616
RESULT 5
ABZ13699 standard; DNA; 2580 BP.
ID ABZ13699 standard; DNA; 2580 BP.
XX
AC ABZ13699;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1504.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
FN W0200216655-A2.
XX
PD 28-FEB-2002.
XX

PF 24-AUG-2001; 2001WO-05026685.
 XX PR 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JF, Krops J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.
 DR Identifying a stress condition to which a plant cell has been exposed and
 XX producing plants with increased tolerance to these abiotic stresses.
 PT Claim 144; SEQ ID NO 1504; 577pp + Sequence Listing; English.
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX SQ Sequence 2580 BP; 778 A; 541 C; 616 G; 645 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,896-293 Length: 2580
 Score: 3202.50 Matches: 595
 Percent Similarity: 82.79% Conservative: 122
 Best Local Similarity: 68.71% Mismatches: 138
 Query Match: 70.63% Indels: 11
 DB: 6 Gaps: 7

US-10-731-642A-1 (1-862) x ABZ13699 (1-2580)

Qy 1 MetPheLeuGluLysValLeuAspAlaIleThrGly-----LysAspGlyLys 17
 Db 1 ATGTTTCGAGAA---CTTAGGATCTGTCACCGCGCGGGAATGAGACGACGAGAG 57
 Qy 18 LysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspLeu 37
 Db 58 AAGGTGAAGAAACGGTCTGATGAAGAAGAAACGCTCTCGATTCAACGATTCAAT 117
 Qy 38 AlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeu 57
 Db 118 GCTTCGTTCTCGATCGCTCATGAATTTCTCGGAAACAAATCACTCTCGTCTGTA 177
 Qy 58 SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLeuArgSerLysAlaAla 77
 Db 178 AGCTCTGATGTTACTGATTCGAAACCGTTCTTAAGGCAAACTAGGGAAGGCTGCTCAC 237
 Qy 78 LeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgVal 97
 Db 238 TTGGAGGATTGGATCACAACAATCAGTCGTTAACCCGCGAGCGAATCCGCTTCAAGTC 297
 Qy 98 ThrPheAspTrpAspAspGluPheGlyValProGlyAlaPheIleLysAsnLeu 117
 Db 298 ACGTTTCGATTAC--GAACCCGATTTCCGCTTACCTCGGAGCATTTTCAAGAACAGC 354
 Qy 118 HisPheSerGluPheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLys 137
 Db 355 CATTCAGTGAGTTCTTCTCAAAAGTCTCACACTTGAAGAGCTTCCAGGCGCATGGCAGA 414
 Qy 138 ValHisPheValCysAsnSerTrpValTrpProAlaAsnLysTrpLysSerAspArgile 157
 Db 157

Db 415 GTCCATTACATCTGTAAATTTCTTGGATTTTACCCTGCTAAACACTACACACTACAGACCGAGTC 474
 Qy 158 PhePheAlaAsnGlnAlaIleThrProSerGluThrProAspThrLeuArgLysTrpArg 177
 Db 475 TTCTTCTCCAAACAGACTTATCTCCACATGAACACACGACGACGCTGCTCAAGTATAGA 534
 Qy 178 GluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluThrPheArg 197
 Db 535 GAAGAAGAGCTAGTGAGTTTGAGAGAACCGCGGAGGAGAGCTTAAGGAATGGGACAGA 594
 Qy 198 ValTrpAspTrpAlaIleThrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSer 217
 Db 595 GTATATGACTATGCTTACTACAAATGATTAGGCGTCCCAACCAAGAAC-----CCA 645
 Qy 218 ArgProValLeuGlyLysSerSerGluTrpProTrpProArgArgGlyArgThrGlyArg 237
 Db 646 CGGCTGTACTTGGAGGACACAGGAGTATCTTACCACAAAGAGGAGAAACCGGCGCG 705
 Qy 238 LysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAsp 257
 Db 706 AAACCAACTAAGAAGATCTCTMAACCGAGAGCAGCTACCGATCACATCGAGCGCTAGAC 765
 Qy 258 IleTrpValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPhe 277
 Db 766 ATATATGTTCCACGAGATGAGAGATTGGACACTTGAAGATGCTCTGATTTCTCTGCTTAT 825
 Qy 278 AlaLeuLysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThr 297
 Db 826 GCTCTAAAGCGATTGCTCAGTTTCATCAACCTGCACCTTGAGGCTGTATTCACCATACT 885
 Qy 298 HisAsnGluPheAspSerPheGluAspValLeuLysLeuGluGlyLysLeuLysLeu 317
 Db 886 CCTAAGAGTTTGAATCTTTTGAAGATGTTCTTAAGATCTATGAAGAAGAAATCGATCA 945
 Qy 318 ProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluLeuLysGlu 337
 Db 946 CCAACCAAGCTTTGATTGATAGTATCGTTAAGAAATATACCGCTTGAGATGTTAAAGGAG 1005
 Qy 338 LeuLeuArgSerAspGlyGluGlyLeuPheLysTrpProThrProGlnValIleGlnGlu 357
 Db 1006 ATATTCAAGACAGATGGCCAGAAATTCCTTAAGTTTCCAGTGCCCTCAGGTCTATCAAGAG 1065
 Qy 358 AspLysThrAlaIleTrpArgThrAspGluPheGlyArgGluMetLeuAlaGlyValAsn 377
 Db 1066 GACAAACTGATCGAGAACAGATGAGAAATTTGCTAGAGAAATTTGGCTGGACTAAAC 1125
 Qy 378 ProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIle 397
 Db 1126 CCGTGTGTTTATTCAACTTCTTAAGGAGTTTCTCCAAAGAGTAAGCTTGACAGTGAATCA 1185
 Qy 398 TyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeu 417
 Db 1186 TACGGTAACCAAGACAGTACAAATCCTAATAAGCCCATAGAACACAAATTTGGATGGACTC 1245
 Qy 418 ThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeu 437
 Db 1246 ACTGTTGAAGAGCTCTGGAGAGGAGGTTGTTTATATTAGACCAATCATGACACATG 1305
 Qy 438 MetProTrpLeuArgArgIleAsnThrSerThrAspThrLysThrTrpAlaSerArgThr 457
 Db 1306 ATGCCATCTTGGAGCGGTAAACACCAACCCAGC--ACCAAGACTTATGCAAGCAGGACA 1362
 Qy 458 LeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuPro 477
 Db 1363 CTTCTGTTCTTGAAGATGATGGGACCTTGAAGCGGTTGGTGATAGACTGAGCTTGCTT 1422
 Qy 478 HisProAspGlyAspGlnPheGlyValAlaValSerLysValTrpThrProAlaAspGlnGly 497
 Db 1423 CATCTTAATGAGAACAAATTTGGAGCAGTGAAGTATATATACCCCTGGT---GAAGGT 1479
 Qy 498 ValGluGlySerIleTrpGlnLeuAlaLysAlaTrpAlaAlaValAsnAspSerGlyVal 517
 Db 1480 GTCTACGACTCGCTATGCGAGCTTGGCTAAGGCTTTTGTGCGGTGTTAAATGACTCCGGAAT 1539

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QY 518 HisGlnLeuLeuSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla 537
Db 1540 CATGAGCTTATTAGCCATGATGATCAAAACACGATGATGAACCGTTGTGATGCC 1599
QY 538 ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg 557
Db 1600 ACAAACACAGAGCTGAGTGTCTTCCACCGGTCTTAAAGCTCCTTGAACCTCATTCCGT 1659
QY 558 GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeu 577
Db 1660 GATACGATGAATATCAATGCACTTCTAGGCAAAATCTTGATCAATGGTGGTATATTT 1719
QY 578 GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp 597
Db 1720 GAAATCACTGTGTTTCCCTTAAATACCCAGGAGATGTCATCTTTTATTACAAAAC 1779
QY 598 ---TtpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616
Db 1780 CACTGGACCTTCCCTGACCAAGCATTACCAGCAGAACTTAAAGAGAGGATGGCGTT 1839
QY 617 GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636
Db 1840 GAGGATCCAGAAGACACACAGGATTCGTCTGAGATAAAAGACTATCTTACGACGTG 1899
QY 637 AspGlyLeuLysIleTyrSerAlaIleLysSerTyrValThrGluTyrCysAsnTyrTyr 656
Db 1900 GATGGCGTTGAGTTGTGTATGCTATTGAATCATGGGTCGAGACTACATTTTCTTGTTC 1959
QY 657 TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTyrTrpLysGluLeu 676
Db 1960 TACAAGATAGAGGAGGATATCCNAACCCACACAGAGCTCCAGCTGTGTGAGAGGTG 2019
QY 677 ArgGluGluGlyHisGlyAspLysAspGluProTyrTrpProLysMetGlnThrVal 696
Db 2020 CGCAGGAAGGTGATGAGACAAAAAGTCAGAACCCATGTGGCTTAAAGTGCACACCCGT 2079
QY 697 GlnGluLeuIleAspSerCysThrIleThrIleTyrIleAlaSerAlaLeuHisAlaAla 716
Db 2080 GAAGAACTGTGTGAGTCTTGACCATCATATTATTTGGGTGGCTTCGTCTTCATGACGT 2139
QY 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736
Db 2140 GTTAACCTTCGACAGCATATCCAGTCTGGGTACCTCCCAACACAGACCCACTATAAGCCGT 2199
QY 737 AsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLys 756
Db 2200 CAGTACATGCCAAAGGAAAAACACTCCAGAGTTTGAAGAACTTGAGAGAACTCTGATAAA 2259
QY 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyLysLeuLeuGlu 776
Db 2260 GTGTTTTTGAAGACCATCACAGCTCAGCTTCAGACTTCTAGGGATATCTCTGATTGAG 2319
QY 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyr 796
Db 2320 ATTCTCTACTCATCTTAGCCAGGAGTCTATTGTCGACAGAGATCTTAAAGAAATGG 2379
QY 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLeuSerAspIle 816
Db 2380 GCGGCTGAGAAAGAACCGTTGGAGCGGTTGAGAAAGTTTGGAGAGAAAGTAAAGAGATT 2439
QY 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProVal 836
Db 2440 GAGAAAGAACTTGATGAGGAGAACGACGACGAGACTCTCAAGAACAGGACTGTGTTGGTT 2499
QY 837 LysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856
Db 2500 AAGATGCCATACACTTATTGTTTCCGAGCAGTGAAGCGGAGTCCACCGGAGGGGAAAT 2559
QY 857 ProAsnSerValSerIle 862
Db 2560 CCAATAGCGTCTCTATC 2577
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RESULT 6
ID ADA67958 standard; DNA; 2580 BP.
XX
AC ADA67958;
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 206.
XX
KW Plant; bacterial infection; fungal infection; viral infection; ds.
XX
OS Arabidopsis thaliana.
XX
PN W02003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
ID Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
FS Claim 6; SEQ ID NO 206; 899bp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to that
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2580 BP; 778 A; 541 C; 616 G; 645 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.89e-293 Length: 2580
Score: 3202.50 Matches: 595
Percent Similarity: 82.79% Conservatve: 122
Best Local Similarity: 68.71% Mismatches: 138
Query Match: 70.63% Indels: 11
DB: Gaps: 7

US-10-731-642A-1 (1-862) x ADA67958 (1-2580)
QY 1 MetPheLeuGluLysIleValAspAlaIleThrGly-----LysAspAspGlyLys 17
Db 1 ATGTTTCGGAGAA---CTTAGGGATCTGCTACCGCGCGCGGAATGAGACGACGACGAAG 57
QY 18 LysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsn 37
Db 58 AAGTGTGAAGAACCGGTGTTCTGATGAAGAGAACCGTCTCGATTTTCAACGATTTCAAT 117
QY 38 AlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIle 57
Db 118 GCTTCGTTTCTCGATCGTCTTCATGAATTTCTCGGAACAAATCCTCTTCGTTCTGTA 177
QY 58 SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyr 77
|||||
|||||
|||||
|||||
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Db 178 AGCTCTGATGTTACTGATTCAGAAACCGGTTCTAAAGGCCAACTAGGGAAGGCTGCTCAC 237
Qy LeuGluAsnTrpLeuThrAsnSerThrProIleAlaGlyGluSerAlaPheArgVal 97
Db 238 TTGGAGGATGGATCAACAATCAGTCGTCTAACCCGAGCGGAATCCGCTTTCAAGGTC 297
Qy 98 ThrPheAspTrpAspGluGluPheGlyValProGlyAlaPheIleIleAsnLeu 117
Db 298 AGGTTTCGATTAC--GAACACCGATTTCGGTTACCTCGGAGCATTCTTGATCAGAAACAGC 354
Qy 118 HisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLys 137
Db 355 CATTTCACTGAGTTTCTCTCAAAAGTCTCACACTTGAAGCGTTTCCAGGCCATGGCAGA 414
Qy 138 ValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIle 157
Db 415 GTCCATTACATCTGTAATCTTGGAAATTACCTCTGCTAAACACTACCTACAGACCGAGTC 474
Qy 158 PhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArg 177
Db 475 TTCTTCTCCAACAAGACTTATCTTCCACATGAACACACCGAGCGCTGCTCAAGTATAGA 534
Qy 178 GluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArg 197
Db 535 GAAGAAGAGCTAGTGAGTTTGAGAGAAACCGCGGAAGGAGAGCTTAAGGAATGGGACAGA 594
Qy 198 ValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSer 217
Db 595 GTATATGACTATGCTTACTACAATGATTAGCGGTCCTCCACCAAGAAC-----CCA 645
Qy 218 ArgProValLeuGlyLysSerGluTyrProTyrProArgArgGlyValGlyThrGlyArg 237
Db 646 CGGCTGTACTTGAGGGACACAGAGATCTTACCCCAAGAGAGAAACCGGGCGG 705
Qy 238 LysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAsp 257
Db 706 AAACCAACTAAGAAGATCTCTCAACCGAGAGAGGCTACCGATCACATCAGCGCTAGAC 765
Qy 258 IleTyrValProAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPhe 277
Db 766 ATATATGTTCCACGAGATGAGAGATTGGACACTTGAAGATGTCGTGATTTCTGCTTAT 825
Qy 278 AlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThr 297
Db 826 GCTCTAAAGCGATGCTCAGTTTCATCCACTGCACCTGAGGCTGTATTCGACGATACT 885
Qy 298 HisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyLysLeu 317
Db 886 CCTAAAGAGTTGATTTCTTTTGAAGATGTTCTTAAGATCTATGAAGAAGGAATCGATCTA 945
Qy 318 ProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGlu 337
Db 946 CCAACCAAGCTTTGATTGATGATGTTTGAAGATATACCGCTTGAGATGTTAAAGGAG 1005
Qy 338 LeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGlu 357
Db 1006 ATATTCAAGACAGATGGCCAGAAATCTTAAGTTTCCAGTCCCTCAGGTCATCAAGAG 1065
Qy 358 AspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsn 377
Db 1066 GACAAAACCTGCTGAGAACACAGATGAGGAATTTGCTAGAGAAATTTGGCTGGACTAAAC 1125
Qy 378 ProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIle 397
Db 1126 CCGTGTGTTATTCAACTTCTTAAGAGAGTTTCTCCAAAGAGTAAGCTTGACAGTGAATCA 1185
Qy 398 TyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeu 417
Db 1186 TACGGTACCAGAACAGTACATCACTATAAAGCCACATAGAACAAATTTGGATGGACTC 1245
Qy 418 ThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisGlyAspIleLeu 437
Db 1246 ACTGTTGAAGAGGCTCTGGAGAGGAGAGGTTGTTTATATTAGACCACCATGACACACTG 1305

Qy 438 MetProTyrLeuAArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThr 457
Db 1306 ATGCCATACTTGGACCGGTAAACACACCACAG--ACCAAGACTTATGCAAGCAGGACA 1362
Qy 458 LeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuPro 477
Db 1363 CTTCTGTTCTTGAAGATGATGGGACCTTGAAGCGTTGGTGATAGAGCTGAGCTTGCT 1422
Qy 478 HisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGly 497
Db 1423 CATCTAATGAGACAAATTTGGAGCAGTGAAGTGAAGTATATACGCCGTG--GAAGGT 1479
Qy 498 ValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyVal 517
Db 1480 GTCTACGACTCGCTATGGCAGTTGGCTAAGCGTTTGTCCGTGTAAATGACTCCGGAAT 1539
Qy 518 HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla 537
Db 1540 CATCAGCTTATTAGCCTGATGCAACACACACGATCGATTGAACCGTTTGTGATTGCC 1599
Qy 538 ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg 557
Db 1600 ACNAACACAGACAGCTGAGTGTCTTCCCGGCTCTTAAAGCTCCTTGAACCTCCTCCGT 1659
Qy 558 GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeu 577
Db 1660 GATCAGATGATATCAATGCACTTGTAGGCAATCTTGATCAATGGTGGTATATTT 1719
Qy 578 GluLeuThrValPheProAlaLysSerMetGluMetSerAlaValValTyrLysAsp 597
Db 1720 GAAATCACTGTGTTCTTCTTAAATACGCCATGAGATGTCTATCTTTTCATTTTACAAAAAC 1779
Qy 598 ---TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616
Db 1780 CACTGGACCTTCCCTGACCAAGCATTACCACAGAACTTAAAAAGAGAGGATGCGCGT 1839
Qy 617 GluAspSerSerProLeuGluIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636
Db 1840 GAGATCCAGAACACACACGATTCCTGCTGAGGATAAAGACTATCTTACCGAGTG 1899
Qy 637 AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyr 656
Db 1900 GATGGCTTGAGTTTGGTATGCTTAAATCATGCGGTCCGAGACTACATTTTCTTGTTC 1959
Qy 657 TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu 676
Db 1960 TACAAGATAGAGGAGGATATCCAAACCGACACAGAGCTCCAAGCTGTGGTGAAGAGGTG 2019
Qy 677 ArgGluGluGlyHisGlyAspLysAspGluProTyrTrpProLysMetGlnThrVal 696
Db 2020 CGCAGGAGGTCATGGACAAAAGTCAGACCATGCTGGCGCTTAAATGCAAAACCGT 2079
Qy 697 GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAla 716
Db 2080 GAAGAACTTGTGAGTCTTGCAACCATATTATTGGGTGGCTTCTGCTCTTTCATCAGCT 2139
Qy 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736
Db 2140 GTTAACCTCGACAGATATCCAGTTGCTGGGTACCTCCCAACACAGACCACTATAAGCGCT 2199
Qy 737 AsnPheMetProGluProGlySerProGlyGluGluLeuLysThrAsnProAspLys 756
Db 2200 CAGTATGCCAAAGAAAACACTCCAGAGTTTGAGAACTTGAGAAATCTCTGATATA 2259
Qy 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776
Db 2260 GTGTTTTGAAGACCATCAGCTCAGCTTCCAGACACTTCTAGGATATCTCTGATTGAG 2319
Qy 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrp 796
Db 2320 ATTCTCTACTACTTCTAGCGAGGCTTATTTGGGACAGAGATTTCTTAAAGATGG 2379

Qy 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle 816
Db 2380 CGGCTGAGAAGAGCGTTGGAGCGTTTCAGAGTTTGGAGAGAAAGTAAAGAGATT 2439
Qy 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProVal 836
Db 2440 GAGAAGAACATTGATGAGAGGACGACGACGAGACTCTCAAGAACAGGACTGGTTTGGTT 2499
Qy 837 LysValProThrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856
Db 2500 AAGATGCCATACACTTATTCTTTCCGAGCAGTGAAGCGGAGTCACCGGAGGGGAATT 2559
Qy 857 ProAsnSerValSerIle 862
Db 2560 CCAATAGCGTCTATC 2577

RESULT 7
ACD28851

ID ACD28851 standard; DNA; 4687 BP.

XX AC ACD28851;

XX DT 27-AUG-2003 (first entry)

XX DE Wine grape lipoxigenase LOX1 DNA.

XX KW Wine grape; ds; lipoxigenase; LOX; flavour; fermented beverage; wine;
KW grape juice; cheese; yogurt; pickle; tissue specificity; timing; gene.

XX OS Vitis vinifera.

XX PN US200303627-A1.

XX PD 13-FEB-2003.

XX PF 16-OCT-2001; 2001US-00978522.

XX PR 16-OCT-2000; 2000US-0241220P.

XX PA (DESC/) DESCENZO R A.

XX PA (IREL/) IRELAN N A.

XX PI Descenzo RA, Ireland NA;

XX DR WPI; 2003-492095/46.

XX DR P-PSDB; ABO19442.

XX PT Novel purified and isolated Vitis vinifera lipoxigenase polypeptide,
PT useful for modifying the flavor of a comestible e.g., a beverage which is
PT a fermentation product, preferably wine.

XX PS Claim 1; Page 14-16; 36pp; English.

XX CC The invention relates to a purified and isolated Vitis vinifera
CC lipoxigenase (LOX) polypeptide. The polypeptide is useful for modifying
CC the flavour of a comestible e.g. a beverage which is a fermentation
CC product, preferably wine. The polypeptide is useful for analysing the
CC effect of LOX polypeptides on flavour production in wine and grape juice.
CC The polypeptide is useful in the production of cheese, yogurt, pickles
CC etc. The polypeptide is also useful in screening assays to identify
CC modulators that modulate the activity of the Vitis vinifera LOX
CC polypeptides. The polynucleotide is useful in heterologous production of
CC pure lipoxigenase enzyme in a protein expression vector and for studying
CC the native level of gene expression in response to environmental or
CC viticultural influences. The cloned gene can be used to produce
CC transgenic plants to modify the level of gene expression to produce
CC optimal levels of lipoxigenase in the grape. Knowledge of Vitis vinifera
CC lipoxigenase coding DNA sequences allows for modification of cells to
CC permit, increase or decrease, expression of endogenous Vitis vinifera
CC lipoxigenase. Such knowledge also permits modification of timing and
CC tissue specificity of LOX expression. The DNA sequence information also
CC makes possible the development through, e.g. homologous recombination or
CC knock-out strategies of grapes that fail to express functional

CC lipoxigenase or that express a variant of Vitis vinifera lipoxigenase.
CC Such plants are useful as models for studying the in vivo activities of
CC Vitis vinifera lipoxigenase and modulators of Vitis vinifera
CC lipoxigenase. The present sequence represents DNA encoding a wine grape
CC lipoxigenase LOX

SQ Sequence 4687 BP; 1342 A; 920 C; 1008 G; 1417 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.53e-286 Length: 4687
Score: 3138.00 Matches: 652
Percent Similarity: 56.19% Conservative: 110
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 69.21% Indels: 502
DB: 9 Gaps: 10

US-10-731-642A-1 (1-862) x ACD28851 (1-4687)

Qy 3 LeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysValLysGlyThr 22
Db 13 CTCTCTTCAATTGTAGTCCATCACTGGGAAATATGAAGAGAGATCGGGAACT 72
Qy 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42
Db 73 ATTGTGTGATGAAGAAGAAATGTGTGGATTTAATGACTTCAATGCACCGGTTGGGAC 132
Qy 43 GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerSerValAsnAla 62
Db 133 CGGGTTTCATGAGCTTTTGGACAGGGAGTCTCTCGACGCTCGTCAGTGTGTTCATGGT 192
Qy 63 AspPro----- 64
Db 193 GATCCTGGTGAGTTTTTTTTTTTTTTTTCCTTCATGTTTTTGTATGATGGGTTGTTG 252
Qy 64 ----- 64
Db 253 AAGTTGGAGGAGAGGAGTTGATACCGTTTTTGTGAGGTCGAGATCGGTTCTGAATTGA 312
Qy 64 ----- 64
Db 313 TGATAGCAATTGGAAAGAGATGTGATTTTGGAAAGAGGCCAAGAGGGTTGTTATCTCA 372
Qy 64 ----- 64
Db 373 GAGATGAGTCAATGACTTTCTTGACATCTTCCATTCACCTGGGCACCTTTTCTTAAGTCT 432
Qy 64 ----- 64
Db 433 TTTGTTTTTGTGTTTGTGTTTTTAATGCTTTTGTGTTTCTACTTCTTCTTCTTTATAT 492
Qy 64 ----- 64
Db 493 TTCTTTTCATCAACCACTATATACATGCCACCTAATCAATGAATTCATGACGCTG 552
Qy 64 ----- 64
Db 553 CCCCTTTTAAAGCCACTAGATCTTGGTGATTTTGTAGTCTTAGATCTTGGGTTAGAT 612
Qy 64 ----- 64
Db 613 TTCCCGAGATTTCACAAAAGTTGAACCTGAATAATTCAATAAAATTTTGGAGATCACTCCTG 672
Qy 64 ----- 64
Db 673 TTGGAGTTAAAGAGAAAGAAATTGCCATAAACCAAGGAGATGAATTTGTGAATATTTC 732
Qy 64 ----- 64
Db 733 TCATACTTCATCATCAATACTGTCGCAAAACAGCCACAGTTTCTGAATAATTCATGCAGC 792
Qy 64 ----- 64
Db 793 AAAGCCACTGCTGCTTGTGTAGCAAGTCCAAGCTCAACATATAAAGCCGTTTTCAACCCAGTG 852

QY 64 ----- 64
DB 853 ATTTTGTGAGAAATACATGTAAATAATCCAGTACCATCTGTTAGTGATGATATTTGAACCTTG 912
QY 65 ----- AlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAs 80
DB 913 TGTGCTCTTTTGTAGCAAAATGGGTTTACAGGGGAAATCTGGGAACACAGCATACTTGAAGA 972
QY 80 nTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAs 100
DB 973 CTGGATTTACCAAAATACTCTTTAACCGCTGGCGAGTCTGCATTTCAAGGTCAAGTTCGA 1032
QY 100 pTrpAspGluGluPheGlyValProGlyAlaPheIleLysAsnLeuHisPheSe 120
DB 1033 CTGG--GATGAGGAGATTGGAGAGCCAGGGCAATTCATAATTAGAAACAATCACCACAG 1089
QY 120 rGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPh 140
DB 1090 TGAGTTTACCTTCAGGACTCTCACTCTTGAAGATGTTCTGGACGTGGCAGAAATTCATT 1149
QY 140 eValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAl 160
DB 1150 TGTTGTAAATTCCTGGGTCTACCTGCTAAGCACTACAAAACCTGACCGGTGTTTCTTCCAC 1209
QY 160 aAsn----- 161
DB 1210 TAATCAGGTAAAGCTAAATTTGCTTGTACTAGGAGTCTGCTGGCAATTTGSCCCAT 1269
QY 162 -----GlnAl 163
DB 1270 TGAGCTTAGGCAAGGAGAATGCTGCTAAAGGAATGTTTATTTATCTGCTGCAGAC 1329
QY 163 aTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValTh 183
DB 1330 ATATCTTCCAAGTGAACACCAAGGCCACTGGCGCAAGTACAGAAAGGGGAACCTGGTGA 1389
QY 183 rLeuArgGlyAspGlyThrGlyLysLeuGluLeuTrpAspArgValTyrAspTyrAlaTy 203
DB 1390 TCTGAGGGAGAGTGAACCGGAGAGCTTAAGGAATGGGATCGAGTGTATGACTATGCTTA 1449
QY 203 rTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGl 223
DB 1450 CTATAATGATTTGGGGAAGCCAGACAGGATCTCAAAATATGCCCGCTGCTGGGAGG 1509
QY 223 ySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys----- 241
DB 1510 ATCTGCAGAGTATCTTATCCAGAGGGGGAAGAACTGGTAGACCACCATCTGAAAAAAGG 1569
QY 241 ----- 241
DB 1570 TAGATATTTGATACAAATTCATATTTCTCTCATGCTTTTATCATAAAGGATGAATA 1629
QY 242 -----ThrAspProAsnSerGluSerArgIleProLe 252
DB 1630 TGATTGATTTCTGCTCTCTTTTAAATTAACAGATCCCAAAACTGAGAGCAGATGCCACT 1689
QY 252 uLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSe 272
DB 1690 TGTGATGAGCTTAAACATATATGTTTCCAAGAGATGAACGATTTGGTCACTTGAAGATGTC 1749
QY 272 rAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAl 292
DB 1750 AGACTTCTGCTGTATGCTTGAATTCATAGTTCAATTCCTTCTCCCTGAGTTTGAGGC 1809
QY 292 aLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGl 312
DB 1810 TCTATGTGACATCACCCCAATGAGTTTGACAGCTTCCAAGATGATTTAGACCTCTACGA 1869
QY 312 uGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLe 332
DB 1870 AGGAGGAATCAAGGTCCAGAGGGGCCCTTTATCGACAAAAATTAAGGACAACATCCCTCT 1929

QY 332 uGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrPr 352
DB 1930 TGAGATGCTCAAGGAACCTTGTGTGGTACCGATGGGGAACATCTCTTCAAGTTCCCAATGCC 1989
QY 352 oGlnValIle-Gln----- 356
DB 1990 CCAAGTCATCAAAAGGTACTGCATACATCTTAATCTTTTGAAGCCAGATTTAT 2049
QY 357 -----GluAspLysThrA 361
DB 2050 ATATTTATTTTTCATAAAATTTGATGACGTTTTTATCATGCTGGAGCAGAGGATGCTG 2109
QY 361 laTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleI 381
DB 2110 CATGAGGACTGACGAAGAATTTGCTAGAGAAATGCTGCTGGACTCAACCCAGTTGTCA 2169
QY 381 leSerArg----- 383
DB 2170 TCCG-TCCTACTCAAGTAAACTACAGCTTCCTTTCAAAATAATTTTAAATGCCCTGTTGT 2228
QY 383 ----- 383
DB 2229 TTTCTGAGAAAAATGGAACTTGGAAAGGCTTCCAGACTTTGTTTTCTTCCCTCCATCTAC 2288
QY 384 -----LeuGlnGluPheProp 389
DB 2289 TGTCTAGCTCTTTCTGATAATTATTGGCTCTTCTACTTTTGTGTTGAAGGAGTTTCTCT 2348
QY 389 roLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluG 409
DB 2349 CAAAAAGCAAGCTGGATCTCTGAAGTTTATGGCAACAAACAGTTTCAATAACCAAGAAC 2408
QY 409 lnIleGluAspLysLeuAspGlyLeuThrIleAspGluAla----- 422
DB 2409 ACATAGAGATCACCTGGATGACCTTACTATAACGAGGT-AACGCTCTTAGGTTCCGTT 2467
QY 422 ----- 422
DB 2468 CTTTCAAACTAAATTTTCAATGTGACATGTTAAATTTTTTTCATTTGGAACACAAGCCAT 2527
QY 423 -----IleLysThrAsnArgLeuPheIleLeuA 432
DB 2528 AGTAACTGAAAAATGCTGCTTTTACTAGGCAATGGAGAGAAGAGGCTATTTCATATTAG 2587
QY 432 snHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysE 452
DB 2588 ATCCCATGATGTTTTCATGCCATACCTGAGGAGGATAAACACA---ACTTCCACGAAA 2644
QY 452 hrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaI 472
DB 2645 CTTAGGCTCAAGGACTCTCTCTTCTTGAAGAGCAGCGAATTTGAAGCCACTGGCGA 2704
QY 472 leGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrT 492
DB 2705 TTGAATTTGAGCTACCAATCTTAATGGGATAAATTCGAGCTGTCACCAAGATATACA 2764
QY 492 hrProAlaAspGlnGlyValGluGlySerIleTyrGlnLeuAlaLysAlaTyrAlaLav 512
DB 2765 CACCAGCTGAAGATGGCGTTGAAGTTCCATTTGGCAGCTGGCTAAAGCTTATGCTGCTG 2824
QY 512 alAsnAspSerGlyValHisGlnLeuLysSerHisTrpLeu----- 525
DB 2825 TGAATGACTCTGGCTATCATCAGCTCTCCAGCCACTGGTA-CGTAATCTCCCAAGGAAA 2883
QY 525 ----- 525
DB 2884 GTGCGTACAGTTGGGCGTAAATCTGAAGCGGGTTATGAATATCTTTGATGTTGTTGCA 2943
QY 526 -----AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerA 544
DB 2944 GGTGGAATACATGCTGCAATTTGAGTTGCAATTCAGGAGGAGGAGGAGGAGGAGGAGG 3003
QY 544 laLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnA 564

Qy	38	AlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuLeu	57
Db	64	GCITCTCTTGTATCGTGTCAATGAGCTTCTTGCGTCTCTCTCCACCTCATC	123
Qy	58	SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyr	77
Db	124	AGCTCTCACCAACCCGACCCGCGCAATGAGAAGAGAGAGACATTGGAAAGACGACAT	183
Qy	78	LeuGluAsnTrpLeuThrAsn---SerThrProIleAlaAlaGlyGluSerAlaPheArg	96
Db	184	CTGGAAAAATGGGTAAACAAAAATAAAACCGTCAGCTAACCGCTGAGGAAACTTCGCTTTGGA	243
Qy	97	ValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleLeuAsn	116
Db	244	GTAACGTTTGATTGG---GACGAGCTCAATGGGACACCGCGTGCATTGTGTATCAAGAAC	300
Qy	117	LeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGly	136
Db	301	CACCACCATAGTCAATTCCTACCTTAAGTCCCTCACCTCCGCGCTCCCTCAT---GGC	357
Qy	137	Lys-----ValHisPheValCysAsnSerTrpValTyrProAlaAsnLys	151
Db	358	GAAGGTGGTGCACCTGCGATACATTTTCATCTGCAATTTTGGATTATACCGAATCATCGA	417
Qy	152	TyrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAsp	171
Db	418	TACCGCTCCGACCGCGTTTCTCTCTTAACAAGGCATATCTTCCAAGTGAACAACCGGAG	477
Qy	172	ThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArgGly---AspGlyThrGly	190
Db	478	CTAATCAAGAGCTAAGAGAAGAAGACTTAAGAATCTTAAGAGCAATGAGAAGGAGGA	537
Qy	191	LysLeuGluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspPro	210
Db	538	GAATTCAAAGAAATGGGACAGAGTTTACGACTACGCTTATTACAACGACTTTGGGTGCTCCT	597
Qy	211	AspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrPro	230
Db	598	GACAAGGGTCTTGACTCAGTTCTGTCGGTCTTTCGGCGGTTTACCTGAGCTGCCTTATCCT	657
Qy	231	ArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIle	250
Db	658	CGCGTGGCAAAACCGCGCGTAATCCACCAATCAGACCCCTAAGTCTGAAGACGAGCTG	717
Qy	251	ProLeuLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLys	270
Db	718	GCITTTACTA---AACCTAAACATATAGCTGCGCAAGGACGAGCGATTATGACCATGTGAAG	774
Qy	271	LeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPhe	290
Db	775	TTTTTCAGACTTCCTCGCTTATGCACTCAAGTCCGTGACTCAAGTGTGTGTCCTTGAGATC	834
Qy	291	LysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeu	310
Db	835	GCCTCTGTTTTCGACAGACCATCAACGAGTTTGACTCCTTCGAAGATGTTTTTTCACCTC	894
Qy	311	TyrGluGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIle	330
Db	895	TATGACGGTAGTATTAAGCTCGCCAAATGGTCACACCATTTTCTAAGCTCCGTGTATGTATC	954
Qy	331	ProLeuGluIleLeuLysGluLeuArgSerAspGlyGluGlyLeuPheLysTyrPro	350
Db	955	CCGTGGAGAGATTTAGAGAGCTAGTTTCGCNAACCGCAGAAACCGGTTCCTTGAAGTATCCC	1014
Qy	351	ThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArg	370
Db	1015	TTGCCTGCATCTCTCAAAAGAGACAGATCGCTTTGGAGGACTGACGAAGAGTTTGTCTCGA	1074
Qy	371	GluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGluPheProLys	390
Db	1075	GAATGTGTCGCGTCTTATTCGGTGGTAGTACCGGTCTTCAAGAAATTTCAACCAAG	1134

Qy		391	SerLysLeuAspPro	LysIleTyrGlyAsnGlnAnsnSerThrIleThrArgGluGlnIle	410
Db		1135	AGCTGTCTGGAC	TCTGC AAAAGTAGTATGGA AACCAACA CTCTTC CATAGCAACAGAGCACATA	1194
Qy		411	GluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIle	430	
Db		1195	GAATCAAAACATGAACCGCCCTCAATGTGCCAAGAAGCTTTTGAAACAGAAATTAAGCTATTATCATA	1254	
Qy		431	LeuAsnHisHisiAspIleLeuMetProTyrLeuArgGileAsnThrSerThrAspThr	450	
Db		1255	TTGGATCATCACGACGCAATTGATGCCTTACC TGACACGGATAAAC--TCAAACAACACT	1311	
Qy		451	LysThrTyrAlaserArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSer	470	
Db		1312	AAAACCTATTGCGACCGCAACCTCTGCTTGTCTTCAAGCAGACGGAACACTTGAAGCCTCTC	1371	
Qy		471	AlaileGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysVal	490	
Db		1372	GCCATAGACTGAGTCTTCCACACGCAACGAGGCAATCATATGGATCGGTGCACAAGATT	1431	
Qy		491	Tyr-Thr-ProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaYrAla	510	
Db		1432	TTCCACACGACAGAAAGGTGTGAGGGATCGTTTGGCAACTCTGTAAGGCTTATGCT	1491	
Qy		511	AlaValasnaspserglyvalhisglinleuleserhistripleuansnthrhisalaala	530	
Db		1492	CGCGTCAATGACTCTCGTTATCATCATGACTTATAAGCCAATTGGTTGCAACCGCATGCGGTG	1551	
Qy		531	IleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLys	550	
Db		1552	ATTGAAACCGTTCATAATTCGCTCCATAGCGACTCAGCGTGGTCTCCATCCGATCCATAAA	1611	
Qy		551	LeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeu	570	
Db		1612	CITCTACATCCTCATTTCCGTGNACATATGAACATCAACGCATTACGCGGTGATGACTC	1671	
Qy		571	IleAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMet	590	
Db		1672	ATAAATCTCAGACGGAGTCTTTGAGAGAACAGTCTTCCCTAGTCGATACGCCATGGAAATG	1731	
Qy		591	SerAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProthrAspleulle	610	
Db		1732	TCCTTCTCAATTACAAAGAAATTTGGTTTTACCGAGCAGCGCTCTCCCAAAGACCTCCCTC	1791	
Qy		611	LysArgGlyValAlaValGluAspSerSerSerProLeuGlyIleArgLeuLeuilleGln	630	
Db		1792	AACAGGAGGTGCTGTTGAGNATCCAAACAGTAGTGAACCGCGCTTAAGCTTCTGTATCGAA	1851	
Qy		631	AspTyrProTyrAlaValaspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThr	650	
Db		1852	GATTACCCGTTTTCGCGTCGACGGTTTTAGAGATTTGGTCAGCGATCAAAACGGGTGCGTCA	1911	
Qy		651	GluTyrCysAsnTyrTyrTyrLysSerAspAspAlaValGlnLysAspThrGluLeuGln	670	
Db		1912	GAGTACTGACATCTTACTACATAATATGACAAACCGTCCAAACCGGATACAGAGATCCCA	1971	
Qy		671	AlaTrpTriplysgluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrp	690	
Db		1972	TCATGTGTGACCGAGCTCGAACCAAGGCCAGCGGCAACACGACACGAGTCATGGTGG	2031	
Qy		691	ProLysMetGlnThrValGlnGluLeuilleAspSerCysThrIleThrIleTrpIleAla	710	
Db		2032	CCTTTCGATGCAAAACCGCGACGACCTTAATCGAAACCTGCACGATCATCATCTGGATCGCC	2091	
Qy		711	SerAlaLeuHisAlaAlaValasnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsn	730	
Db		2092	TCGTGCTCTTCAGCACACAGTAAATTTTCGACACAGTACCCCTTACGCGCGTTTCTCCCTAAC	2151	
Qy		731	AtqProThrLeuSerArgAsnPheMetProGluPuProGlySerProGluTyrGluGluLeu	750	
Db		2152	CGTCCCTACCGCTACGCGCGGTTTTATGCTCTGAACACGAGTACCGATGAGTATGCTGAGCTG	2211	
Qy		751	LysThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeu	770	

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Db 2212 GAGGAAGTCTGAGTAGCTCTTGAAGACGATCACGCCGAGTTACAGACTCTACTT 2271
Qy 771 GlylleSerLeuIleGluIleuSerArgHisSerAspThrLeuTyLeuGlyGln 790
Db 2272 GGTATCTCCATCATAGAGATATTGCTATGATTCACAGCAGAGATCTACTTAGGGCAA 2331
Qy 791 ArgGluSerProGluTrpThrIleAspGlnGluProLeuSerAlaPheAlaArgPheGly 810
Db 2332 AGAGATTCCACGAATTGACCGCGGATGATGAGCTTTGGAGGGCTTTAAACGGTTTGGG 2391
Qy 811 LysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLys 830
Db 2392 AAAGAACTTGAGCTAGAGACAAATATTATACGAAGAAACAATGACAGAGGTTCAAG 2451
Qy 831 AsnArgSerGlyProValLysValProTyThrLeuLeuPhePro----- 845
Db 2452 AACAGAACCGGACCGGTTAAACATACCGTACACATTTGTTGATCCCGAATACTACGGATTAT 2511
Qy 846 ThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
Db 2512 ACGAGAGAGGTGGGATTACTGGGAAGGATCCCGAAGAGTGTCTCAATC 2562
RESULT 9
ID AAL57712 standard; cDNA; 2929 BP.
XX
AC AAL57712;
XX
XX 06-NOV-2003 (first entry)
XX
DE Balsam pear (Momordica charantia) lipoxxygenase isozyme 2 cDNA.
XX
KW Lipoxxygenase; hydroperoxidation; polyunsaturated fatty acid; plant;
KW fatty acid metabolite synthesis; signal molecule; growth regulation;
KW development regulation; plant development; wound response;
KW genetic mapping; hyperoxidation catalysis; Balsam pear; gene; ss.
XX
OS Momordica charantia.
XX
FH Key Location/Qualifiers
FT CDS 12..2654
FT /tag= a
FT /product= "Balsam pear lipoxxygenase 2"
XX
XX US2003074693-A1.
XX
PN 17-APR-2003.
XX
XX 29-JAN-2002; 2002US-00059909.
XX
XX 10-FEB-1999; 98US-0119597P.
XX 09-FEB-2000; 2000US-00501422.
XX
XX (CAHO/) CAHOON E B.
XX (KINN/) KINNEY A J.
XX (KLEI/) KLEIN T M.
XX (LEEJ/) LEE J.
XX (PEAR/) PEARLSTEIN R W.
XX (RAFA/) RAFALSKI J A.
XX (SHEN/) SHEN J B.
XX (THOR/) THORPE C J.
XX (TING/) TING S V.
XX (WENG/) WENG Z.
XX
XX Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;
XX Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;
XX
XX WPI: 2003-567325/53.
XX P-PSDB; AAO27492.
XX
XX New isolated polynucleotides encoding plant lipoxxygenases, useful in
XX genetic mapping, particularly in catalyzing hyperoxidation of
PT
```

```
PT polyunsaturated fatty acids.
XX
XX Claim 6; Page 22-23; 36pp; English.
XX
CC This invention relates to novel nucleotide sequences which encode
CC proteins which have lipoxxygenase activity. Lipoxxygenases are membrane
CC bound ubiquitous enzymes which catalyze the hydroperoxidation of
CC polyunsaturated fatty acids in the first step of fatty acid metabolite
CC synthesis. Products of this pathway are found as signal molecules
CC involved in growth and development regulation. A knowledge of the amino
CC acid sequence of lipoxxygenases may allow the understanding of plant
CC development and wound response. The polynucleotides, polypeptides and
CC lipoxxygenases of the invention may therefore be useful in genetic mapping
CC and particularly for catalyzing hydroperoxidation of polyunsaturated
CC fatty acids. The present sequence is the cDNA sequence which encodes the
CC Balsam pear (Momordica charantia) lipoxxygenase protein 2 of the invention
XX
XX Sequence 2929 BP; 910 A; 587 C; 662 G; 770 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 6.92e-276 Length: 2929
Score: 3022.50 Matches: 554
Percent Similarity: 80.99% Conservative: 132
Best Local Similarity: 65.41% Mismatches: 156
Query Match: 66.66% Indels: 5
DB: 9 Gaps: 4
US-10-731-642A-1 (1-862) x AAL57712 (1-2929)
Qy 16 GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp 35
Db 126 GGGAGAGAGATCAAGGGGACGGTGTCTTATGAGAGCAATGTTTGGACTTCACCGAA 185
Qy 36 IleAsnAlaSerValLeuAspGlyValLeuPheLeuGlyArgArgValSerLeuGlu 55
Db 186 TTTCAATCTCTCATTCTTGTACGGGTCTCAGCTCTTGGCGCGGAAATTTCAATTGCAA 245
Qy 56 LeuIleSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAla 75
Db 246 CTTATCAGTGTCTACTACGCT-----TCCAAACACTCCGAGGGAAGTTGGAAAGGGG 299
Qy 76 AlaTyLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPhe 95
Db 300 GCGTTTCTGGAGAGGTGGCTGACTTCAGTTCGCCCACTGTTTCGCTGGAGAGTCTGTGTT 359
Qy 96 ArgValThrPheAspTrpAspAspGluPheGlyValProGlyAlaPheIleIleLys 115
Db 360 CAAGTGAACCTTGATTGG--GAAGAGAACTTTGGATTCCAGGAGCTTTCTTCATAAAA 416
Qy 116 AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis 135
Db 417 AATGGGCACACCACTGAGTCTTCTCAAGTCTGTACTCTGGAGGATGTTCTCGGCTTT 476
Qy 136 GlyLysValHisPheValCysAsnSerTrpValTyProAlaAsnLysTyLysSerAsp 155
Db 477 GGAAGGGTCCATTTTGACTGCACTCATGGGTTTTACCCCTCTCGAAGATCAACAAGAT 536
Qy 156 ArgIlePhePheAlaAsnGlnAlaTyIleuProSerGluThrProAspThrIleuArgLys 175
Db 537 CGCATTTTCTTTGGCAACCATACATGCTTCCAATCGATACACCGGATTCATCTCGTAAG 596
Qy 176 TyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrp 195
Db 597 TATAGAGAGGAGGAGTGTGTGAACCTCAGAGAGATGGACAGGAGAGCGTAAGATGG 656
Qy 196 AspArgValTyAspTyAlaTyTyAsnAspLeuGlyAspProAspLysGlyGlnAsp 215
Db 657 GATAGATTTTATGACTATGATGTTTACAAACACCTCTGTGATCCAAATGGTGTCTTAAC 716
Qy 216 LeuSerArgProValLeuGlyGlySerSerGluTyProTyProArgArgGlyArgThr 235
Db 717 CTTGTTCTGCTCTATTCTTGGAGGAGTGTATCAGTACCTTACCTTCCTCGTAGAGGGAGACA 776
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Db	1851	AAGGAATGGAAGTTCCCGATGAAGCAGCTCCCTACTAAATCTCAATTAAAGAGAGTAGCA	1910
Qy	616	ValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAla	635
Db	1911	ATTGAGAGCTCAGGCTCTCCCATGAGTTCGACTTCTTAATAACGATTAACCCCTTGCT	1970
Qy	636	ValAspGlyLeuIlystleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyr	655
Db	1971	GTTGATGGGCTCGAGATTTGGTCAGCCATCAAAACATGGGTACACAGATTACTGCTCCCTC	2030
Qy	656	TyrTyrIlysserAspAlaValGlnIlyAspThrGluLeuGlnAlaTrpTrpLysGlu	675
Db	2031	TACTTACAAAGACGACGACGCAATTCGAAATGATGTGCGAGCTCCAAATCATGGTGGGAAGAA	2090
Qy	676	LeuArgGluGluGlyHisGlyAspLysLysAspGluProTyrTrpProLysMetGlnThr	695
Db	2091	CTCAGAGAAAGAGTCTATACAGACAGAAAGACGAGCCATGTGGGGCCAAATATGCAAACT	2150
Qy	696	ValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAla	715
Db	2151	TTTTTCAGAGTTAATTGAATCATGCACCATTAATCATATGGATTTCCTCAGCCCTTCAGCA	2210
Qy	716	AlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSer	735
Db	2211	GCAGTCAAATTTTGGGCAATACCCCTTATGGAGGCTACGTTCCCAACAGACCAACCAAGC	2270
Qy	736	ArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAsp	755
Db	2271	AGAAGATTATCCGCAAGTAGGACTGCAGAGTACAAAGAGTTGAATCAAAACCCCTGAA	2330
Qy	756	LysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIle	775
Db	2331	AAGGCCTTTCTAAGACAAATCAGCTCGCAATAGTAGTGCTCTCTTGGCCTCTCGATAAT	2390
Qy	776	GluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGlu	795
Db	2391	GAATAATGTGCAAGCAGCGCTTCTGACGAGGTCTACTCGGGCAAGAGCCAGCATTGAG	2450
Qy	796	TrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAsp	815
Db	2451	TGACATCATGACAAATCTGCAATGAAGCCTTTGAGAAATTTGGGAAGAGCTGTTTGAA	2510
Qy	816	IleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyPro	835
Db	2511	GTTGAGGATAGATTATGCGAAGGATCAAGATGTGAACTTGAGAAATCGAGTGGGCCT	2570
Qy	836	ValLysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGly	855
Db	2571	GTCAATATGCTTACACTTGTCTTGTTCATCGAGTACTGAGGAGCTACTCTGGGAGAGGA	2630
Qy	856	IleProAsnSerValSerIle 862	
Db	2631	ATTCCCAACAGTATCTCCATA 2651	
RESULT 10			
AAF88022			
ID	AAF88022 standard; DNA; 2964 BP.		
AC	AAF88022;		
XX			
DT	13-JUL-2001 (first entry)		
XX			
DE	Cucumber LBLOX DNA SEQ ID 3.		
XX			
KW	Cucumber; LBLOX; fatty acid metabolism; lipid metabolism;		
KW	plant oil-production; transgenic plant; ds.		
XX			
OS	Cucumis sativus.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	48..2684	
FT		/*tag= a	

FT /product= "LBLOX"

XX DE19950921-A1.

XX PD 26-APR-2001.

XX 21-OCT-1999; 99DE-01050921.

XX 21-OCT-1999; 99DE-01050921.

XX (BADI) BASF AG.

XX Kindl H, May C, Feussner I;

XX WPI; 2001-274658/29.

XX P-PSDB; AAB86036.

XX New isolated nucleic acid encoding sequence that targets proteins to lipid bodies, useful for producing transgenic plants for lipid and fatty acid production.

XX Claim id; Page 14-18; 30pp; German.

XX This invention describes a novel isolated nucleic acid sequence (I), encoding a polypeptide, comprising a sequence (Ia) involved in fatty acid or lipid metabolism, and a targeting sequence (Ib). (I) are used to produce oil-producing transgenic plants or eukaryotic microorganisms, for production of lipids or derived fatty acids. This sequence encodes a Cucumis sativus (cucumber) LBLOX protein which is described in the method of the invention

XX Sequence 2964 BP; 988 A; 516 C; 583 G; 877 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.64e-265	Length:	2964
Score:	2911.00	Matches:	534
Percent Similarity:	78.65%	Conservative:	140
Best Local Similarity:	62.31%	Mismatches:	175
Query Match:	64.20%	Indels:	8
DB:	4	Gaps:	6

US-10-731-642A-1 (1-862) x AAF88022 (1-2964)

QY 6 lleValAspAlaIleThrGlyLysAspGlyLysValLysValLysGlyThrValValLeu 25

DB 135 ATTTAGTAGAGTTTCCAGTCTT---GGAGGAACAATAATCAAGGGAAGTGAATCTT 191

QY 26 MetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAspGlyValLeu 45

DB 192 ATGAGAAGCAATGTTTGGATTCTCACTGAATTCATTCCAAATCTTCTTGATAACTTCACT 251

QY 46 GluPheLeuGlyArgValSerLeuGluLeuIleSerSerValAsnAlaAspProAla 65

DB 252 GAGCTCTGGGTGGTGTCTTCTTCCAACTCATTAGTGCCACTCATACT-----TCA 305

QY 66 AsnGlyLeuGlnGlyLeuArgSerLysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSer 85

DB 306 AATGACTCAAGAGGGAAGATTGGGAACAGGCAATATTGGAGAGGTGGCTAATCTTCAATC 365

QY 86 ThrProIleAlaAlaGlySerAlaPheArgValThrPheAspTrpAspGluGlu 105

DB 366 CCACCACTGTTTGGTGGAGAATCAGTGTTCCAAAATCAACTTTTCAATGG---GATGAAAT 422

QY 106 PheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhePheLeuLys 125

DB 423 TTTGGATTTCAGGAGCTTCTTCATAAAAAATGGACATACAAAGTGAATCTTCTTCAAA 482

QY 126 SerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCysAsnSerTrp 145

DB 483 TCTCTCACTCTTGATGATGTTCTGCTGATGAGAGTCCATTTGATTCGAATCTTCTGG 542

QY 146 ValTyrProAlaAsnLysThrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeu 165

DB 543 GTTTACCCCTTCTGGAAGATACAGAAAGATCGCATTTTCTTTGCGCAATCATGTTTATCTT 602

QY 166 ProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArg 185

DB 603 CCAAGTCAACACACCAACCCCTCTTCGTAAGTATAGAGAGGAAGAAATTGTGAAATTTGAGA 662

QY 186 GlyAspGlyThrGlyLysLeuGluGluTyrAspArgValTyrAspTyrAlaTyrTyrAsn 205

DB 663 GGAGATGGACAGAGGAAGAAAGAAATGGATGAGAAATTTATGACTATGATGTTTATAT 722

QY 206 AspLeuGlyAspProAspLysGlyLysAspLeuSerArgProValLeuGlyGlySerSer 225

DB 723 GACATTGCTGACCTGATGTTGGTGAT-----CATGCTCTATTCTCGGTGGACGACC 776

QY 226 GluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsn 245

DB 777 GAATATCTTACCCTCGTAGGGGAAGAACAGGACGACCATCATCAAGAAGAGACCAAT 836

QY 246 SerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArgAspGluArg 265

DB 837 TATGAGAGCAGATTGTCCACCAATATGAGTTAGCATCTATGATCCCAAAAGATGAAAC 896

QY 266 PheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeu 285

DB 897 TTTGGCATTGGAAGATGTGAGATTCTCTGTTATACATATAAAGCACTTTTCGATATCA 956

QY 286 LeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGlu 305

DB 957 ATCAAAACAGGAGCTTCATTCATATTGATGTAATCTCAAAATGAATTTGACAAATTTTAAA 1016

QY 306 AspValLeuLysLeuTyrGluGlyLysLeuProGlnGlyProLeuLeuLysAla 325

DB 1017 GAAGTTGATATATCTCTTTGAGAGAGTTTCCCATTTCCATTAT---GCTTTAAGACC 1073

QY 326 IleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGly 345

DB 1074 CTCAGTGGGACCTCACTCCACCTTTGTTCAAGCACTCGTGAGGAATGATGTTGAAAAA 1133

QY 346 LeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAsp 365

DB 1134 TTCTCAAAATTTCTACTCCGGAAGTTGTCAAGATATAAATAAGGATGAGGACACTGAT 1193

QY 366 GluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGln 385

DB 1194 GAAGAAATTTCAAGAGAAATGTTAGCAGGACCCATCTCTATTGATTCGTCGTTGAA 1253

QY 386 GluPheProLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIle 405

DB 1254 GCTTTTCCCAACAAGTAAGCTTGACCAATGTTTATGGGAATCAAAACAGTACCATC 1313

QY 406 ThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThr 425

DB 1314 ACTGAAGAACAACATAAAGCATGGTTTAGTGGTCTTACGGTGTAGGCAATGAAGCAA 1373

QY 426 AsnArgLeuPheIleLeuAsnHisIleAspIleLeuMetProTyrLeuArgArgIleAsn 445

DB 1374 AACAGGCTCTACATAGTGGATTTCATGATGATTAATGCCCTATCTTACAAGGATGAT 1433

QY 446 ThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGly 465

DB 1434 ---GCAATCAACAAAAACATATGCCAAGAAATGAGTTCCTTTTGAAGATGATGGG 1490

QY 466 ThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGly 485

DB 1491 ACTTTGAAGCCATTGGTTAATGATGCTTGGCATCTCTCAAGGAGATCAACTTGGT 1550

QY 486 AlaValSerLysValTyrThrProAlaAspGlnGlyValGlySerIleTrpGlnLeu 505

DB 1551 GCCATTAGCAACATATCTTTCCAGCTGAAATGGAGTTCAAAATCCATTGGCAATTG 1610

QY 506 AlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuLeuSerHisTrpLeu 525

DB 1611 GCTAAAGCTTATGAACCTGTTAATGATGTTGGTACCATCACTATTATTAGTCATTGGTTG 1670

Qy 526 AsnThrHisAlaAalleleGluProPheValIleAlaThrAsnArgGluLeuSerAlaLeu 545
 Db 1671 CATACTCATGCTGACTTGTAGCCATTGTGATGCAACATAGACAATTTGACGTGCTT 1730
 Qy 546 HisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeu 565
 Db 1731 CATCCAAATCCATAAGTGTGCTTCTCTCATTAACAAAGACATATGTTTATAAATCATCT 1790
 Qy 566 AlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLys 585
 Db 1791 GCAAGACAAGTTTTCATCAATGCCAATGCTCTATCGAACAACCCATTCATCAACAAA 1850
 Qy 586 TyrSerMetGluMetSerAlaValValTyrLysAspTyrValPheProGluGlnAlaLeu 605
 Db 1851 TATTCATAGGAGTGTCTATCTATCTGTACAGGATTTGACCTTCCTGATCAACATTA 1910
 Qy 606 ProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerProLeuGlyIle 625
 Db 1911 CCTAATAATCTCATGAGAGGAGTGTAGTGTGGAGGACTCAAGTGTCCCTCATGACTT 1970
 Qy 626 ArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTyrSerAlaLeu 645
 Db 1971 AGATTGCTAATAAATGATATCATCTTGTGTGTGATGCTTGTGACATTTGGTCAGCCATT 2030
 Qy 646 LysSerTyrValThrGluTyrCysAsnTyrTyrTyrLysSerAspAlaValGlnLys 665
 Db 2031 AAACATGGGTACAGGATTTTGTCTCTACTACAAAGATGACATGACATCAAAAT 2090
 Qy 666 AspThrGluLeuGlnAlaTyrTrpLysGluLeuArgGluGluGlyHisGlyAspLysLys 685
 Db 2091 GACTTTGAATCCATCTTGTGGTGAATGAGCTAAGAGAGAGGCGCCGCTGACAAGAA 2150
 Qy 686 AspGluProTyrTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIle 705
 Db 2151 CATGAACCATGCTGCGCAAAATGCAAACTTTAAGTGAATTAATCGAATCTCTGCACTACA 2210
 Qy 706 ThrIleTyrIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAla 725
 Db 2211 ATTATATGATGCTTCTAGCTCTTCATGCCGAGTTAACTTTGGACAAATATCCCTACGGA 2270
 Qy 726 GlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerPro 745
 Db 2271 GGCTATATTTCAATCGACCACTACAAGTGTGCTGATGCTTCAATGAGTGGCAGCGCT 2330
 Qy 746 GluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGln 765
 Db 2331 GAGTACAAAGAACTGGAATCGAATCCGAAAGAGCTTTCTTGAGAACAAATATGTTTCAGAA 2390
 Qy 766 LeuGlnThrLeuGlyLysSerLeuIleGluLeuSerArgHisSerSerAspThr 785
 Db 2391 TTACAGACATGTTGATGATTTCAATATTTGAATTTGTAAGATGCTTCTGATGAA 2450
 Qy 786 LeuTyrLeuGlyGlnArgGluSerProGluTyrThrLysAspGlnGluProLeuSerAla 805
 Db 2451 GTTATCTTGACAAGAGCTTCAATGATGAGCTTCAGATAAATTCGATTCGAGCA 2510
 Qy 806 PheAlaArgPheGlyLysLysLysSerAspIleGluAspGlnIleMetGlnMetAsnVal 825
 Db 2511 TTTGAGAAATTTGGGAAAAATTTATTTGAAGTTGAGATAGCATCATGGAAGGAATAAA 2570
 Qy 826 AspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThrLeuLeuPhePro 845
 Db 2571 GAGGTGAATTTGAAGAATAGATCTCGACCTGTGAATTTGGCTTATCTACTCTTCTTCCA 2630
 Qy 846 ThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
 Db 2631 TCAAGTACGAGGACTCACTGGAAGAGGAATCTCTAATAGTATTTCTATC 2681
 RESULT 11
 ID ABX13453
 XX ABX13453 standard; DNA; 2964 BP.

AC ABX13453;
 XX 04-JUN-2003 (first entry)
 XX C. sativus lipoygenase DNA corresponding to Genbank X92890.
 XX Expression cassette; transgenic; promoter; LOX5; plant; food production;
 KW animal feed; seed; stress resistance; disease resistance; starch content;
 KW lipid content; dormancy; fibre content; pharmaceutical production;
 KW fine chemical production; sterile plant; vitamin; flavouring; perfume;
 KW dye; cotyledon; embryonic tissue; stress factor; LOX; ds.
 XX Cucumis sativus.
 XX DE10127882-A1.
 XX 12-DEC-2002.
 XX 11-JUN-2001; 2001DE-01027882.
 XX 11-JUN-2001; 2001DE-01027882.
 XX (BADI) BASF PLANT SCI GMBH.
 XX Bischoff F, Feussner I, Loyall LP;
 XX WPI; 2003-279966/28.
 XX Cassette for expressing transgene, useful e.g. in production of
 PT pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
 of Arabidopsis, provides cotyledon-specific expression.
 XX Claim 5; Page; 28pp; German.
 XX This invention describes a novel cassette for the transgenic expression
 of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
 thaliana or deletion variants of the LOX5 promoter which are functionally
 linked to the nucleic acid of the invention. The cassette is used to
 prepare transgenic organisms, especially plants, for production of foods,
 animal feeds, seeds (including those with increased resistance to stress
 and disease, altered starch/lipid contents or dormancy, or altered fibre
 content), pharmaceuticals (especially antibodies, vaccines, enzymes and
 pharmaceutical proteins) and fine chemicals (especially enzymes,
 vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,
 perfumes and dyes), also to produce sterile plants. The LOX5 promoter
 provides strong and specific expression in cotyledons and/or other early
 embryonic tissue, so can degrade, or protect against, stress factors to
 which these tissues are particularly sensitive. Since cotyledons are the
 main storage organs of seeds, expressing transgenes in them produces
 targeted increases/modifications in nutritional value. Expression in the
 cotyledons is homogeneous, there are no side effects on other plant
 organs (pollen) and the promoter is functional in a wide variety of
 plants (ornamentals or crops). This sequence represents a nucleic acid
 sequence associated with the Arabidopsis thaliana LOX gene described in
 the disclosure of the invention
 XX Sequence 2964 BP; 988 A; 516 C; 583 G; 877 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.64e-265 Length: 2964
 Score: 2911.00 Matches: 534
 Percent Similarity: 78.65% Conservative: 140
 Best Local Similarity: 62.31% Mismatches: 175
 Query Match: 64.20% Indels: 8
 DB: 6
 US-10-731-642A-1 (1-862) x ABX13453 (1-2964)
 Qy 6 ileValAspAlaIleThrGlyLysAspGlyLysValLysGlyThrValValLeu 25
 Db 135 ATTTAGATGAGTTTCCAGTCTT---GGAGGAACAAATCAAGGGAAGTATCTT 191
 Qy 26 MetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAspGlyValLeu 45

Db 192 ATGAGACCAATGTTTGGATTTCACTGAATTCATTCATTCCTCTTGATAACTTCACT 251
Qy 46 GluPheLeuGlyArgValSerLeuGluLeuLeuSerSerValAsnAlaAspProAla 65
Db 252 GAGCTCTTGGGTGGTGGTCTTCTTCAACTCAATAGTGCACATCACTACT-----TCA 305
Qy 66 AsnGlyLeuGlnGlyLysArgSerLysAlaAlaValLeuGluAsnTrpLeuThrAsnSer 85
Db 306 AATGACTCAAGAGGGAAGATTGGGAACCAAGGATATTTGGAGAGTGCTTAATCTTCAATC 365
Qy 86 ThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAspGluGlu 105
Db 366 CCACCACTGTTTGGTGGAGATCACTGTTCCAAATCAACTTTCATGG--GATGAAT 422
Qy 106 PheGlyValProGlyAlaPheIleLeuLysAsnLeuHisPheSerGluPhePheLeuLys 125
Db 423 TTTGGATTTCCAGGAGCTTCTTCATATAAAATGACATACAAAGTGAATTTCTTCTCAA 482
Qy 126 SerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCysAsnSerTrp 145
Db 483 TCTCTCACTCTTGATGATGTTCTCGCTATGCGAGAGTCCATTTTGATGGCAATTCCTGG 542
Qy 146 ValTrpProAlaAsnLysTrpLysSerAspArgIlePhePheAlaAsnGlnAlaTrpLeu 165
Db 543 GTTTACCTTCTGGAAGATACAAAGAAAGATCGCAATTTCTTGGCCAATCATGTTATCT 602
Qy 166 ProSerGluThrProAspThrLeuArgLysTrpArgGluAsnGluLeuValThrLeuArg 185
Db 603 CCAAGTCAACACCAACCAACCTCTCGTAAGTATAGAGAGGAAGAATTTGTGGAATTTGAGA 662
Qy 186 GlyAspGlyThrGlyLysLeuGluTrpAspArgValTrpAspTrpAlaTrpTrpAsn 205
Db 663 GGAGATGGAAACAGGAGGAAGAAGAAATGGGATAGAAATTTATGACTATGATTTTATAAT 722
Qy 206 AspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSer 225
Db 723 GACATGCTGACCTGATGTTGGTGTAT-----CATGCTCTTATCTCGTGGGAGGACC 776
Qy 226 GluTrpProTrpProArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsn 245
Db 777 GAATATCTCTTACCTCGTAGGGGAAGAAACAGGACGACCAACAGGAGAGACCAACAT 836
Qy 246 SerGluSerArgIleProLeuLeuMetSerLeuAspIleTrpValProArgAspGluArg 265
Db 837 TATGAGACGAGATGTCACCAATATAGCTTAGACATCTATGTACCAAAAGATGAAGAAC 896
Qy 266 PheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeu 285
Db 897 TTTGGGCATTTCAAGATGTCAGATTTCTTGGTTATACATTAAGACACTTTTCGATATCA 956
Qy 286 LeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGlu 305
Db 957 ATCAAAACGAGGACTTCAATCCCATATTTGATGTAACTCCAAATGAATTTGACAAATTTAA 1016
Qy 306 AspValLeuLysLeuTyGluGlyIleLysLeuProGlnGlyProLeuLeuLysAla 325
Db 1017 GAAGTTGATAATCTCTTGAGAGAGGTTTCCCATTTCCATTTAAAT---GCTTTTAAAGACC 1073
Qy 326 IleThrAspSerIleProLeuGluLeuLysGluLeuLeuArgSerAspGlyGluGly 345
Db 1074 CTCACCTGAGGACTCACTCCACTTGTTCMAAGCACTCGTGAGGAATGATGTTGAAGAAA 1133
Qy 346 LeuPheLysTrpProThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAsp 365
Db 1134 TTTCCCTCAAAATTTCTACTCCCGAAGTTGTCAAGATAATAAAATAGGATGGAGCACTGAT 1193
Qy 366 GluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleLeuSerArgLeuGln 385
Db 1194 GAAGAAATTTGCAAGAGAAATTTAGCAGGACCAATCCCTCTATTTGATTCGTCTTTGAA 1253
Qy 386 GluPheProProLysSerLysLeuAspProLysIleTrpGlyAsnGlnAsnSerThrIle 405

Db 1254 GCTTTTCCACCAACAAGTAAGCTTGACCCAAATGTTTATGGGAATCAAAAACAGTACCATC 1313
Qy 406 ThrArgGluGlnIleGluLeuAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThr 425
Db 1314 ACTGAAGAACACATAAAGCATGGTTTAGATGGTCTTACGGTTGATGAGCAATGAAGCAA 1373
Qy 426 AsnArgLeuPheIleLeuAsnHisIleAspIleLeuMetProTrpTrpLeuArgIleAsn 445
Db 1374 AACAGGCTCTACATAGTAGGATTCATGATGATTAATGATCCCTATCTTACAAGGATGAAT 1433
Qy 446 ThrSerThrAspThrLysThrTrpAlaSerArgThrLeuLeuPheLeuGluAsnAsnGly 465
Db 1434 ---GCAACATCAACAAACAAATATGCCACAAGAACATTTCTTTTGAAGATGATGGG 1490
Qy 466 ThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGly 485
Db 1491 ACTTTGAAGCCATTTGGTTATTTAGCTTGCCACATCTCTCAAGGAGATCAACTTGGT 1550
Qy 486 AlaValSerLysValTrpThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeu 505
Db 1551 GCCATTAGCAAACTATATCTTTCCAGCTGAAATGGAGTTCAAAATCCATTTGGCAATTG 1610
Qy 506 AlaLysAlaTrpAlaAlaValAsnAspSerGlyValHisGlnLeuLysSerHisTrpLeu 525
Db 1611 GCTAAAGCTTATGTAACCTGTTAATGATGTTGGCTACCATCACTTATTAGTCATTGGTTG 1670
Qy 526 AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeu 545
Db 1671 CATACTCAATGCTGACTTTGAGCCATTTGTGATTTGCAACATAGACAAATTTGAGCGTCT 1730
Qy 546 HisProIleTrpLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeu 565
Db 1731 CATCAATCCATAGTTGCTGTTCTCTTACAAAGACACTATGTTTATAATGCATCT 1790
Qy 566 AlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuValPheProAlaLys 585
Db 1791 GCAAGACAAGTTTGTATCAATGCCAATGCTCTTATCGAAACAACCCATTTATCCATCAAAA 1850
Qy 586 TyrSerMetGluMetSerAlaValValTrpLysAspTrpValPheProGluGlnAlaLeu 605
Db 1851 TATTCAATGGAGTTGTGATCTATCTTTGACAAAGATGGACCTTCCCTGATCAGACATTA 1910
Qy 606 ProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSerProLeuGlyIle 625
Db 1911 CCTAATAATCTCATGAGAGAGGACTAGCTGTGGAGGACTCAAGTGCCTCCCATGGACTT 1970
Qy 626 ArgLeuLeuIleGlnAspTrpTrpAlaValAspGlyLeuLysIleTrpSerAlaIle 645
Db 1971 AGATTGCTAATAAATGATTTATCCATTTGCTGTGATGGTCTTTGACATTTGGTCAGCCATT 2030
Qy 646 LysSerTrpValThrGluTrpCysAsnTrpTrpTrpLysSerAspAlaValGlnLys 665
Db 2031 AAAACATGGGTACAGGATTTATGCTGCTCTTACTACAAAGATGACATGCGATGACAAAT 2090
Qy 666 AspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGlyHisGlyAspLysLys 685
Db 2091 GACTTTGACTCCATCTTTGGTGAATGAGCTAAGAGAAAGGCCACGCTGACAAGAAA 2150
Qy 686 AspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIle 705
Db 2151 CATGAACCATGCTGGCCAAAATGCAAACTTTTAAAGTGAATTAATCGAATCTCGCACTACA 2210
Qy 706 ThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTrpProTrpAla 725
Db 2211 ATTATGATGATGCTTTCAGCTCTTATGCCGAGTTTAACTTTGGACAATATCCCTACGGA 2270
Qy 726 GlyTrpLeuProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerPro 745
Db 2271 GGTATATTTCTCAATCGACCAACTACAAGTCGTAGTTCATGCTTCAAGTGGCAGCGCT 2330
Qy 746 GluTrpGluGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGln 765
Db 2331 GAGTACAAAGAACTCGAATCGAATCCGAAAAGCTTTTCTTGAGAACATATATGTTTCAGAA 2390

WPI; 2003-874315/81.
P-PSDB; ABW02705.

New maize lipoxigenase polynucleotide, designated CSSAP92, useful for altering lipoxigenase concentration in plants, for decreasing accumulation of aflatoxin in plants, or for increasing the resistance of plants to pathogens.

Claim 1; SEQ ID NO 1; Opp; English.

The invention relates to maize lipoxigenase polynucleotide, designated CSSAP92. The nucleic acid molecule and methods are useful in altering lipoxigenase concentration in plants, in decreasing accumulation of aflatoxin in plants, or in increasing the resistance of plants to pathogens. The invention is useful in gene therapy. The present sequence is the maize lipoxigenase cDNA

```
Db 1796 TTCCGGCGCAGTACCGCTGGCGATGCTCCGGTGGTGTACAGAGCTGGAACCTTCACC 1855
Qy 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSer 621
Db 1856 GAGCAGGGCTTCCCGCGACCTGCTCAAGAGGGCGTGGCGGTGGCGGACCCGCTCCAGC 1915
Qy 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuIle 641
Db 1916 CCGTACAAGGTGGCGCTGCTGATCAGAGACTACCCGTACGCGAGCGAGCGGTGGCCATC 1975
Qy 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661
Db 1976 TGGCAGCGCATCGACAGTGGTGGCGAGTACCTGGCCATCTACTACCCGACGACGGC 2035
Qy 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHis 681
Db 2036 GCGCTCGGGCGGACGAGAGCTGCGAGCGTGGTGAAGGAGGTGCGGAGGTGGCGGAC 2095
Qy 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701
Db 2096 GCGCACCACAAAGGACCGCCCTGGTGGCCCAAGATGCAAGGCGGTGTCGAGGCTGCCACG 2155
Qy 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721
Db 2156 GCGTCACACCATCATCTGGATCGCTGGCGGCTCCAGCGCCGCTCACTTCGCGCAG 2215
Qy 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741
Db 2216 TACCGGTACGGGGGTACTCTCCGAACAGGCCACGGTGAGCGCGCGCGGATGCGGAG 2275
Qy 742 ProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLysThr 761
Db 2276 CCGCGCACAAAGGAGTACGAGAGCTGAGCGCGCGAGCGCGCGGCTTCATCCACACC 2335
Qy 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781
Db 2336 ATCAGAGCCAGATCCAGACCATCATCGGCATCTCGCTCATCGAGATCTCTCCAGCAC 2395
Qy 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGlu 801
Db 2396 TCCTCCGACGAGGTACTCTCGCGCAGCGCAGCACCCCGAGTGAGCTCCGACGCCCGG 2455
Qy 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821
Db 2456 CGCCTGGCGCGGTTCAGAGGTCTCAGCAGCGCTGGTCAAGATCGAGGGCAAGGTGGT 2515
Qy 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841
Db 2516 GCGGAGAACCGGACCCGACGCTGAGGAACAGGAACGCGCCCGCGAGTTCCTCATATG 2575
Qy 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855
Db 2576 CTGCTCTATCCCAACACCTCTGACCACAGTGGCGCGCGCGAGGGCTCACTGCCAAGGCG 2635
Qy 856 IleProAsnSerValSerIle 862
Db 2636 ATCCCAACAGCATCTCCATC 2656

RESULT 14
ID ADG93380
XX ADG93380 standard; DNA; 2595 BP.
XX
AC ADG93380;
XX
DT 11-MAR-2004 (first entry)
XX
DE Maize lipoxigenase (LOX) DNA #6.
XX
KW Maize; lipoxigenase; LOX; corn; gene; ds; plant;
KW plant pathogen defence system; plant development; tissue healing;
KW mycotoxin; aflatoxin; sterigmatocystin.
XX
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OS Zea mays.
XX
FN US2003168855-A1.
XX
PD 04-SEP-2003.
XX
PF 25-APR-2002; 2002US-00132350.
XX
PR 27-APR-2001; 2001US-0286889P.
PR 13-JUL-2001; 2001US-0305366P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Navarro Acevedo PA, Duvick JP, Kolomiets MV, Simmons CR;
XX
DR WPI; 2003-898106/82.
XX
DR P-PSDB; ADG93381.
XX
PT New lipoxigenase polypeptides and polynucleotides, useful for enhancing
PT resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for
PT promoting healing of damage tissues, or for modulating plant growth and
PT development.
XX
PS Disclosure; SEQ ID NO 11; 151pp; English.
XX
PS The invention relates to maize lipoxigenase (LOX) polypeptides and
XX polynucleotides encoding the polypeptides. The LOX polypeptides and
XX polynucleotides are useful in modulating plant pathogen defence systems
XX (particularly enhancing resistance to fungi, viruses, nematodes and
XX insects) and plant development, and for promoting healing of damaged
XX tissues. LOX proteins may also be used to inhibit the production of
XX mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing
XX fungus in plants susceptible to contamination by the mycotoxins. This
XX sequence represents DNA encoding a maize LOX polypeptide of the
XX invention.
XX
SQ Sequence 2595 BP; 505 A; 925 C; 802 G; 363 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,69e-252 Length: 2595
Score: 2769.50 Matches: 524
Percent Similarity: 74.74% Conservative: 124
Best Local Similarity: 60.44% Mismatches: 208
Query Match: 61.08% Indels: 11
DB: Gaps: 5

US-10-731-642A-1 (1-862) x ADG93380 (1-2595)
Qy 3 LeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysValLysGlyThr 22
Db 4 CTGAGCGGGATCATCGACGGCTGACGGGGCGGAACAGCATGCGCGCTCAAGGGCAG 63
Qy 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42
Db 64 GTGGTGTCTATGTCGCAAGACGTGCTGACCTCAACGACTTCGGCGCCACCGTCTGTGAC 123
Qy 43 GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerSerValAsnAla 62
Db 124 AGCATCAGCGAGTTCTCTCGCAAGGGGTCACTGCGCAGCTCATCAGCTCCACCTCGTC 183
Qy 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82
Db 184 GACGCCAACAAACGCAACCGCGGGGTGCGGGCGGAGGCGAACCCTGGAGCAGTGGCTG 243
Qy 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
Db 244 ACAGACCTGCGCTGCTGACGACCGCGGAGTCCAAAGTTCCGGCTCACGTTCCACTGGAG 303
Qy 103 AspGluGluPheGlyValProGlyAlaPheIleLysAsnLeuHisPheSerGluPhe 122
Db 304 GTGGAGAGAGCTGGGAGTGGCGGGGGCGCTCGTCTCAAGAAACAACCCACCGCGCGAGTTC 363
Qy 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
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QY	856	IleProAsnSerValSerIle 862	Db	128	GTGGTGTCTCATGCGCAAGAACGTCGTGGACCTCAACGACTTCGCGCGCCACCGTCGTTGAC 187
Db	2572	ATCCCAACAGCATCTCCATC 2592	QY	43	GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerSerValAsnAla 62
RESULT 15			Db	188	AGCATCAGCGAGTTCTCTCGCAAGGGGTCACTGCGCAGCTCATCAGCTCCACCCCTCGTC 247
ADG93378			QY	63	AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82
ID ADG93378			Db	248	GACGCCAACACGCGAACCCGCGCGGGTGGGGCGGAGCGAACCTCGAGCAGTGGCTG 307
XX			QY	83	ThrAsnSerThrProIleAlaAlaGlyLysAlaPheArgValThrPheAspTrpAsp 102
DT	11-MAR-2004	(first entry)	Db	308	ACGAGCTCGCGTCCGCTCAGCACCGCGAGTCCAAAGTTCCGCGCTCAGCTTCGACTGGAG 367
XX			QY	103	AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122
DE		Maize lipoxigenase (LOX) DNA #5.	Db	368	GTGGAAGAGTGGGAGTCCCGGGGCGCTCGTCAAGAACCAACCGCCCGCGAGTTC 427
KW		Maize; lipoxigenase; LOX; corn; gene; ds; plant;	QY	123	PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
KW		plant pathogen defence system; plant development; tissue healing;	Db	428	TTCTCAAGACAATCACCCTCGACGACGTGCCGCGCGCGCGCTCACCTTCGTCGCC 487
KW		mycotoxin; aflatoxin; sterigmatocystin.	QY	143	AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162
XX		Zea mays.	Db	488	AACTCTGGGTCTACCCCGCGGCAAGTACCGCTACAACCGCGTCTTCTTCTCCAACGAT 547
PN	US2003166855-A1.		QY	163	AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182
XX	04-SEP-2003.		Db	548	ACGTACCTGCCAAGCCAGATCCCGCGCGCTGAAGCCGTACCGCGGACGACGAGTCCGC 607
PF	25-APR-2002; 2002US-00132350.		QY	183	ThrLeuArgGlyAspGly--ThrGlyLysLeuGluGluTyrAspArgValTyrAspTyr 201
PR	27-APR-2001; 2001US-0286889P.		Db	608	AACCTCCCGCGGACGACGACGAGCCCTTACAGGAGCAGCAGCGGTGTACCGCTAC 667
PR	13-JUL-2001; 2001US-0305366P.		QY	202	AlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeu 221
XX	(PION-) PIONEER HI-BRED INT INC.		Db	668	GACGTCTACAACGACCTCGCGGAGCCCGACGCGGCAAC-----CCGCGCCCATCTCTC 721
PT		New lipoxigenase polypeptides and polynucleotides, useful for enhancing	QY	222	GlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys 241
PT		resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for	Db	722	GCGGCTCCGCGGACCCCGTACCCGCGCGCTCCGCGGCGCGCGCGCGCGCGCGCGCG 781
PT		promoting healing of damage tissues, or for modulating plant growth and	QY	242	ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValPro 261
XX		development.	Db	782	ACCGACCCCACTCGGATAGCGACTGTGCTGGTGAG-----CAGATCTACGTGCGG 835
PS	Disclosure; SEQ ID NO 9; 15ipp; English.		QY	262	ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281
CC		The invention relates to maize lipoxigenase (LOX) polypeptides and	Db	836	CGGACGAGCGCTTCGCGCACCTCAAGATGTCGACTTCTCTGGGCTACTCCATCAAGGCC 895
CC		polynucleotides encoding the polypeptides. The LOX polypeptides and	QY	282	IleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPhe 301
CC		polynucleotides are useful in modulating plant pathogen defence systems	Db	896	ATCAGCAGGGGATCATCCCGCGGTGCGCAGCTACGTGGACACCCACCCCGCGGAGTTC 955
CC		(particularly enhancing resistance to fungi, viruses, nematodes and	QY	302	AspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGlyPro 321
CC		insects) and plant development, and for promoting healing of damaged	Db	956	GACTCTTCAGGACATCATCAACTGTACAGAGGCGGGATCAAGTGCCTCAAGATCCAG 1015
CC		tissues. LOX proteins may also be used to inhibit the production of	QY	322	LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341
CC		mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing	Db	1016	GCGCTCGAGGACATCGCAAGCTCTTCGCGCTCCAGCTCGTCAAGGACCTCTCTCCCGCGC 1075
CC		fungus in plants susceptible to contamination by the mycotoxins. This	QY	342	AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGluAspLysThrAla 361
CC		sequence represents DNA encoding a maize LOX polypeptide of the	Db	1076	GCGGGGACTACCTGCTCAAGCTCCCATCCACAGATCATCCAAAGAGCAACGAACGCG 1135
XX		invention.	QY	362	TrpArgThrAspGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIle 381
SQ	Sequence 3007 BP; 656 A; 1012 C; 887 G; 452 T; 0 U; 0 Other;		Db	1136	TGAGGACCGACAGGAGTTCCGCGGAGGTGCTCGCGCGGTCAACCCGATGGTGATC 1195
Alignment Scores:			QY	382	SerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGln 401
Pred. No.:	7.07e-252	Length: 3007	Db	1196	ACGCGCTCAGGAGTTCCGCGGCAAGGACGCTGGACCCCGCAAGTACGCGGACAC 1255
Score:	2769.50	Matches: 524			
Percent Similarity:	74.74%	Conservative: 124			
Best Local Similarity:	60.44%	Mismatches: 208			
Query Match:	61.08%	Indels: 11			
DB:	10	Gaps: 5			
US-10-731-642A-1 (1-862) x ADG93378 (1-3007)					
QY	3	LeuGluLysIleValAspAlaIleThrGlyLysAspAspGlyLysLysValLysGlyThr 22			
Db	68	CTGACGGGATCATCAGCGGCTGACGCGGGCGCAACAGCATGCGCGCTCAAGGCGACG 127			
QY	23	ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42			

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QY 402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421
DB 1256 ACCAGCAGCATCAGCGGAGGACATCGAGAGAACTCGAGGCGCTCAGGTGAGCAG 1315
QY 422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrLeu 441
DB 1316 GCGCTGAGCGGCAACAGGCTTACATCTCTGGACCAACAGCAGCGCTTACGCGTTCCTC 1375
QY 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461
DB 1376 ATCGACGTCAACACCTGAGGGTAACCTCATCTACGCCACCAAGGACCTCTTCTTCCTG 1435
QY 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481
DB 1436 CCGCGGAGCGGAGGCTCGCGCCCTCGCTATCGAGCTCAGCGAGCGCTACATCGACGGG 1495
QY 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501
DB 1496 GACCTTACCGTGCCCAAGAGCAAGGTCTACAGCGCGCGCTCCAGCGCGCTCGAGGCGCTGG 1555
QY 502 IleTropGlnLeuAlaIleAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521
DB 1556 GTGTGGCAGCTCGCCAAAGCGCTATGTGCGCGTCAACGACTCTGGCTGGCCACCAACTCGTC 1615
QY 522 SerHisTropLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGln 541
DB 1616 AGCCACTGGCTGACACGCGGCGGTGATGGAGCGCTTCTGTATCGCGACGAAACCGGAG 1675
QY 542 LeuSerAlaLeuHisProTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561
DB 1676 CTGAGCGTGACGACCCGCGTGCACAAAGCTCTCTGAGCTGCACCTTCGCGACACCATGACC 1735
QY 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThrVal 581
DB 1736 ATCAACGCGCTCGCGCGGAGACGCTCATCAACGCGCGCGGCTATCTTCGAGATGACCGTC 1795
QY 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTyrValPhePro 601
DB 1796 TTCCCGGGCAAGTACGCGCTGGCATGTCTCTCGTGGTGTACAGAGCTGGAACTTCACC 1855
QY 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSer 621
DB 1856 GAGCAGGGGCTCCCGCGCCACCTCGTCAAGAGGGCGTGGCGGTGGCGGACCGTCCAGC 1915
QY 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641
DB 1916 CTGTACAAGGTGCGGCTGTGATCGAGGACTACCCGTACGAGCGACGCGGCTGGCCATC 1975
QY 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661
DB 1976 TGGCAGCCATCGAGCAGTGGGTGGCGAGTACCTGGCCCATCTACTACCCCGACGACGCG 2035
QY 662 AlaValGlnLysAspThrGluLeuGlnAlaIleTrpTrpLysGluLeuArgGluGlyHis 681
DB 2036 GCGCTGCGGGGCGACGAGGAGCTGACGAGCGTGTGGAGAGGCTGGCGGAGTGGGGCAC 2095
QY 682 GlyAspLysLysAspGluProTyrTrpProLysMetGlnThrValGlnGluLeuLeuAsp 701
DB 2096 GCGCACCACAAAGGACGCGCCCTGGTGGCCCAAGATGACGAGCGGCTGTGGAGCTCGCCAGC 2155
QY 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721
DB 2156 GCGTGACCAACCATCATCTGGATCGGCTCGGCGCTCCAGCCGCGCGTCAACTTCGGCCAG 2215
QY 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741
DB 2216 TACCCGTACGCGGGGTACCTCCGAAACAGCGCCACGCTGAGCGCGCGCGATGCGGAG 2275
QY 742 ProGlySerProGluTyrGluGluLysThrAsnProAspLysValPheLeuLysThr 761
DB 2276 CCGCGGACGAGAGTACGAGGAGCTGGAGCGGACCGCGGAGCGCGGCTTCATCCACACC 2335
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QY 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781
DB 2336 ATCAGAGCCAGATCCAGACCATCATCGCTCATCGAGATCTCTCTCCAAGCAC 2395
QY 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGlu 801
DB 2396 TCCTCCGACGAGGTGTACCTCGGCCAGCGCGACACCCCGAGTGGACCTCCGACGCGCG 2455
QY 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821
DB 2456 GCGCTGGCGCGGCTTCAAGAGGTTACGACGCGCTGGTCAAGATCGAGGCGAAGTGGTG 2515
QY 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841
DB 2516 GCGGAGAAACCGGACCCGCGAGCTGAGGAACAGGAACGCGCGCGAGTTCCCTTACATG 2575
QY 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855
DB 2576 CTGCTCTACCCCAACACCTCTGACCAACAGTGGCGCGCGCGAGGCTCACTCCCAAGGC 2635
QY 856 IleProAsnSerValSerIle 862
DB 2636 ATCCCAACAGCATCTCCATC 2656
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Search completed: March 14, 2005, 06:02:38
Job time : 1196 secs

A vertical ruler scale showing measurements from 0 to 6 inches. The markings are as follows:
- 0 inch: at the bottom.
- 1 inch: 8 small tick marks above 0.
- 2 inch: 16 small tick marks above 0.
- 3 inch: 24 small tick marks above 0.
- 4 inch: 32 small tick marks above 0.
- 5 inch: 40 small tick marks above 0.
- 6 inch: 48 small tick marks above 0.
The numbers 1 through 6 are placed to the right of their respective inch marks.

45 ATGCTCTTTGGGTGAATTTGGATGCCATCTCTTGAAAGAGATGATAGCCAAAAGTGAAA 104
Db
21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40
Qy
105 GGAAGAGTGAATTTGATGAAAAAATGTTCTAGACCTTCATTAATATAGGTGCTTCAGTT 164
Db
41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuLeuSer---Ser 59
Qy
165 GTTGATGGCAATTTCTGATTTACTTGGCCAAAGTCTCTATCCAAATGATAGTGGTTCT 224
Db
60 ValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysLeuAlaAlaValrLeuGlu 79
Qy
225 GTTAATTATGAT-----GGTTTGAAGGAAACTGAGCAATCCAGCATACTTAGAG 275
Db
80 AsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99
Qy
276 AGTTGGCTTACAGACATCACCCCAATAACAGCAGGGGAATCAACTTTTAGTGTGTACATTT 335
Db
100 AspTrpAspAspGluGluPheGlyValProGlyAlaPheIleLeuLysAsnLeuHisPhe 119
Qy
336 GACTGGGATCGTGCAGGTTTGGAGTTCCAGGAGCATTCATCATCAAGAACTTCATCTT 395
Db
120 SerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHis 139
Qy
396 AATGAGTCTCTTCTCAAGTCACTCACACTCGAAGATGTTCTCTAATTATGGAATAATCCAT 455
Db
140 PheValCysAsnSerTrpValrProAlaAsnLysTyrrLysSerAspArgIlePhePhe 159
Qy
456 TTTGATGCAATTTCTGGGTATCTGCTGCTTTTAGATACAAGTCTGACCGCATTTTCTTT 515
Db
160 AlaAsnGlnAlaTyrrLeuProSerGluThrProAspThrLeuAlaGlyLysTyrrArgGluAsn 179
Qy
516 GCCAATCAGGCTTATCTCCAGTGAACACACCAACCATTCGGAATAATACAGAGAAAT 575
Db
180 GluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValrTyrr 199
Qy
576 GAACGTGTAGCTTTGCGAGGAGATGGAATCGAAGCTTGAAGATGGGACAGGGTTTAT 635
Db
200 AspTyrrAlaTyrrAsnAspLeuGlyAspProAspLysGlyGluAspLeuSerArgPro 219
Qy
636 GATTATGCTGTGACAACTGAGTGGTGAACACAGATAAGGGGAAAGATGCTAGGCGCT 695
Db
220 ValLeuGlyGlySerSerGluTyrrProTyrrProArgArgGlyArgGlyLysPro 239
Qy
696 ATCTTTGGAGGTCTCTGAGTACCGGTATCTCTGAGGAGGAGACAGGCCCGCAACA 755
Db
240 ThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrr 259
Qy
756 ACCAAAGCAGATCTCTAAATGCGAGAGCAGGAACCCATTGCTATGAGCTTAGACATATAT 815
Db
260 ValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeu 279
Qy
816 GTCCCAAGGAGCAGCGATTTGGTTCATGTGAAGAGTCAAGCTTTTGACGTCGCTCTTA 875
Db
280 LysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsn 299
Qy
876 AAATCTCTTTTCCAAACGCTTCTCTGCTTAAAGCTTTTGGCGATAACAGCCTAAT 935
Db
300 GluPheAspSerPheGluAspValLeuLysLeuTyrrGluGlyIleLysLeuProGln 319
Qy
936 GAGTTCAATAGCTTTTGGCGATGTACTTAATCTCTATGAAGGAGGAATCAAGTTGCTGAA 995
Db
320 GlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeu 339
Qy
996 GGCCTCTGGTTGAAAGCCATTAATGATTAATCTCTCAGAGATTAATAAGACATCTCT 1055
Db
340 ArgSerAspGlyGluGlyLeuPheLysTyrrProThrProGlnValIleGlnGluAspLys 359
Qy
1056 CAACCGATGTCAGGCCCTTCTTAAGTACCCAACTCTCAGGTATTATCAAGCGCATAAA 1115
Db
360 ThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProVal 379
Qy
1116 ACTGCATGAGGACGATGAAGAAATTTGGAGAGAAATGTTGGCAGGATCCCAATCTCTGTC 1175
Db

380 IleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrrGly 399
Qy
1176 TTAATAGTAGTACCCCAAGAAATTTCTCCGAAGAGCAGTGGATCCCAACCATATATGA 1235
Db
400 AsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIle 419
Qy
1236 AACCAAAACAGTACAATACCAAGACATGTACAGGATAGTTGAATGGATTAAACAGTG 1295
Db
420 AspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIleLeuMetPro 439
Qy
1296 AATGAGGCAATCAAGAGTAACAGGTATTATCATTTGAACCAACCATGACATCGTATGCCA 1355
Db
440 TyrrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrrAlaSerArgTrpLeuLeu 459
Qy
1356 CTATTGGAGAAATTAACATGTCCAGCAACAAAGCCATATGCTCAAGAACTCTGTGTC 1415
Db
460 PheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisPro 479
Qy
1416 TTCTCTACAGATGATAGNACTTTGAGCCACTAGCAATTTGAATTAAGCTTGCCACATCCA 1475
Db
480 AspGlyAspGlnPheGlyAlaValSerLysValrTyrrProAlaAspGlnGlyValGlu 499
Qy
1476 GACGAGATCAATTTGGTACTGTTAGTAAAGTATATACACAGCTGACCAAGGTGTTGAA 1535
Db
500 GlySerIleTrpGlnLeuAlaLysAlaTyrrAlaAlaValAsnAspSerGlyValHisGln 519
Qy
1536 GGTCTATCTGCGAGTTTGGCAAGCCCTATGTAGCAGTGAATGACATGGGCATTCATCAG 1595
Db
520 LeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsn 539
Qy
1596 CTCTATTAGCCACTGTTGCAATACACACGCGGTGATCGAACCATTTGTGATTGCAACAAT 1655
Db
540 ArgGlnLeuSerAlaLeuHisProIleTyrrLysLeuLeuHisProHisPheArgGluThr 559
Qy
1656 AGGCATCTAAGTGTGCTTCATCCCATTCATAAACTTCTTCATCTCATTTCCGTAACACG 1715
Db
560 MetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeu 579
Qy
1716 ATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTATGATGGTGGT---TTTGAGACG 1772
Db
580 ThrValPheProAlaLysTyrrSerMetGluMetSerAlaValValrTyrrLysAspTrpVal 599
Qy
1773 TCTCTTTTCTGCGCAAAATATTCATGGAATGTGACAGCAGCTTACAAAGATTGGGT 1832
Db
600 PheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSer 619
Qy
1833 TTCCCTGAACAGCACTTCTGCTGATCTCTCAAAAGAGGAGTGGCTGTTGAGGACTTG 1892
Db
620 SerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrrProTyrrAlaValAspGlyLeu 639
Qy
1893 AGCTCCCAACATGCAATTCGTTTACTGATCTGACATATCCATATGCTGTTGATGGCTTG 1952
Db
640 LysIleTrpSerAlaIleLysSerTrpValThrGluTyrrCysAsnTyrrTyrrLysSer 659
Qy
1953 GAAATTTGGCGAGCAATCAAAAGTTGGTAAAGAAATATTCAGATTTCTATTACAAATCT 2012
Db
660 AspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGlu 679
Qy
2013 GACGAGACAGTAGAGAAAGACACTGAATCTCAAGCTTGGTGAAGGAGCTCCGCGAAGAA 2072
Db
680 GlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeu 699
Qy
2073 GGACATGCGCAAGAAAGATGAGCTTGGTGGCTTAAACTGCAAACTCGCAAGAGCTC 2132
Db
700 IleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPhe 719
Qy
2133 AGAGATTGTCACCATCATTTATGATAGCTTTCAGCACTTCATGACGACTCCCATTTT 2192
Db
720 GlyGlnTyrrProTyrrAlaGlyTyrrLeuProAsnArgProThrLeuSerArgAsnPheMet 739
Qy
2193 GCCTTATCTCTAGCTGGTGTATCTCCCTAATCGCCCTACTTTAAGCTGTAATTTGATG 2252
Db

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QY 740 ProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeu 759
Db 2253 CAGAGCCAGGAGTGTGAGTATGAGAGCTCAAGACAAATCCAGACAAAGGTATCTTA 2312
QY 760 LysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluLeuSer 779
Db 2313 AAAACATTTGTTCCCTCAGTTGCAATCAGTCTTGAAATTTCCATCTTTGAGGCTCGTCA 2372
QY 780 ArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluThrLysAsp 799
Db 2373 AGCGATGCTTCAGATGAGGTTTACITGGACAAAGGAGCTCAATGAAATGGCAAAAGGAT 2432
QY 800 GlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGln 819
Db 2433 AAAGAACCACCTGTAGCTTTTGAGAGGTTTGGAAAGATCTTAAGTATCGAATCGA 2492
QY 820 IleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValPro 839
Db 2493 ATTATGATAAATGAATAGTCATAGAGTTTGGAAAGACAGGTCAGGGCCTGTTAAACGTTCCA 2552
QY 840 TyrThrLeuPhePheProThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSer 859
Db 2553 TATACGTTGCTCTTTCCCAAGTGAAGAGGAGCTCACAGGCAAAAGGAATCCCAACAGT 2612
QY 860 ValSerIle 862
Db 2613 GIGTCTATA 2621

RESULT 2
US-09-051-465-4
; Sequence 4, Application US/09051465A
; Patent No. 6355862
; GENERAL INFORMATION:
; APPLICANT: Handa, Avtar K.
; APPLICANT: Kausch, Kurt D.
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits
; FILE REFERENCE: 7024-297
; CURRENT APPLICATION NUMBER: US/09/051,465A
; PRIORITY FILING DATE: 1998-07-31
; APPLICATION NUMBER: PCT/US96/16387
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: 60/005,404
; PRIOR FILING DATE: 1995-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: ASCII
; SEQ ID NO 4
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-051-465-4

Alignment Scores:
Pred. No.: 0 Length: 2871
Score: 3625.50 Matches: 685
Percent Similarity: 87.49% Conservative: 70
Best Local Similarity: 79.37% Mismatches: 103
Query Match: 79.96% Indels: 5
DB: 3 Gaps: 3

US-10-731-642A-1 (1-862) x US-09-051-465-4 (1-2871)

QY 1 MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysValLys 20
Db 45 ATGTCTTTGGTGGGAATTTGATGTCATCTTGGAAAAAGATGATAGGCAAAAGTGAAA 104
QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40
Db 105 GGAAGAGTGTATTTGAIGAAAAAAGTTCATAGATCTTCATTAATATAGGTCCTCAGTT 164
QY 41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuLysLeuIleSer---Ser 59
Db 165 GTTGATGGCATTTCTGATTTACTTTGGCCAAAAAGTCTCTTCAATTTGATAAGTGTTCT 224
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QY 60 ValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGlu 79
Db 225 GTTAATATGAT-----GGTTTGAAGGGAACCTGAGCAATCCAGCATACTTAGAG 275
QY 80 AsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99
Db 276 AGTTGGCTTACAGACATCACCCCAATAACAGCAGGGAATCAACTTTTAGTGTTCATTT 335
QY 100 AspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPhe 119
Db 336 GACTGGGATCGTACAGAGTTTGGAGTTCAGAGACATTCATCAAGAATCTTCATCTT 395
QY 120 SerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHis 139
Db 396 AATGAGTCTTCTCAAGTCACTCACACTCGAAGATGTTCTTAATATGAAAAATCCAT 455
QY 140 PheValCysAsnSerTrpValTrpProAlaAsnLysTrpLysSerAspArgIlePhePhe 159
Db 456 TTTGATGCAATTTCTTGGGTTTATCTCTGTTTATAGATACAAGTCTGACCGCATTTCTTT 515
QY 160 AlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTrpArgGluAsn 179
Db 516 GCCAATCAGGCTTATCTCCCAAGTGAACACCAACCATTCGAAAAATACAGAGAAAT 575
QY 180 GluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyr 199
Db 576 GAATCTGAGCTTTTCGAGGAGATGGAAGTTCGAAAGCTTGAAGATGGACAGGGTTAT 635
QY 200 AspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgPro 219
Db 636 GATTATGCTTGCTACAAATGACTTGGTGAACCAAGATGAAGGGGAAGATGATGCTAGGCT 695
QY 220 ValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysPro 239
Db 696 ATCTCTGGAGGGTCTCTGAGTACCGCTATCTCTGAGGAGGAGGAGGAGGAGGAGGAG 755
QY 240 ThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyr 259
Db 756 ACCAAAGCAGATCTTAATTCGAGAGCAGGAGCAACCATTCCTATGAGCTTAGCATATAT 815
QY 260 ValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeu 279
Db 816 GTCCCAAGGAGCAGGAGGATTTGGTCAATGTGAAGAAGTCAGACTTTTGACGCTGCTTA 875
QY 280 LysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsn 299
Db 876 AAATCCTCTTTGCAAAACGCTTCTCTCGGTTTAAAGGCTTTGTCGATAACACGCTAAT 935
QY 300 GluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuProGln 319
Db 936 GAGTTCATAGCTTTGCGAGTACTTAATCTCTATGAAGGAGGAATCAAGTTGCTGAA 995
QY 320 GlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLysLeuLeuLeu 339
Db 996 GGCCCTTGGTTGAAAGCCATTACTGATAACATTTCTCTCAGAGATACTAAAAGACATCTT 1055
QY 340 ArgSerAspGlyGluGlyLeuPheLysTrpProThrProGlnValIleGlnGluAspLys 359
Db 1056 CAAACGGATGTCAGAGGCTTACTTAAGTACCAACTCTCTCAGGTTATTTCAGCGGATAAA 1115
QY 360 ThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProVal 379
Db 1116 ACTGATCAGAGCAGGATGAAGATTTGGAGAGAAATTTGGCAGGATCCATCTCTGTC 1175
QY 380 IleIleSerArgLeuGlnGluPheProTrpLysSerLysLeuAspProLysIleTyrGly 399
Db 1176 TTAATCAGTAGACTCCAAGATTTCTCCGAAGAGCAAGTTCGATCCCAACCATATATGA 1235
QY 400 AsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIle 419
Db 1236 RAACCAAAACAGTACAAATTTACCACAGAACATGTACAGGATAAGTTGAATGATTAACAGTG 1295
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QY 420 AspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHsiAspIleLeuMetPro 439
Db 1296 AATGAGGCAATCAAGAGTAACAGGTTATTCATATTGAACCAACCATGACATCGTGAATGCCA 1355
QY 440 TyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeu 459
Db 1356 CTATTGAGGAAATTAACATGTCAGCAAAACACAAAAGCCTATGCTCAAGAACTCTGCTC 1415
QY 460 PheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisPro 479
Db 1416 TTCTTACAGATGATAGAACCTTTGAAGCCACTAGCAATTTGAATAGCTTGCACATCCA 1475
QY 480 AspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGlu 499
Db 1476 GACGAGATCAATTTGGTACTGTTAGTAAAGTATATACACAGCTGACCAAGGTGTTGAA 1535
QY 500 GlySerIleTTPGlnLeuAlaLysAlaTyrAlaIaValAsnAspSerGlyValHisGln 519
Db 1536 GGTTCATCTGGCAGTTTGCCAAAGCCTATGTAGCAGTGAATGACATGGCATTCTATCAG 1595
QY 520 LeuIleSerHisTTPLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsn 539
Db 1596 CTCATTAGCCACTGTTGAATACACACGCGGTGATCGAACCATTTGTGATTCACAAAT 1655
QY 540 ArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThr 559
Db 1656 AGGCATCTAAGTGTCTCATCCCAATTCATAACTTCTTCATCTCATTTCCGTAACAG 1715
QY 560 MetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuLeuLeu 579
Db 1716 ATGAACAATAATGCTTTAGCAAGAGACACCTTGACTATGATGGTGGT---TTTCAGAGC 1772
QY 580 ThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTTPVal 599
Db 1773 TCTCTTTTCTCCGCCAAATATTCATGGAAATGTCTAGCAGCAGCTTACAAAGATTGGGT 1832
QY 600 PheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSer 619
Db 1833 TTCCCTTGACAGACTTCTCTGCTGATCTCTCAAGAGAGGAGTGGCTGTTGAGGACTTG 1892
QY 620 SerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeu 639
Db 1893 AGCTCCCAACATGGCATTCGTTACTGATTCTGGACTATCCATATGCTGTTGATGGCTTG 1952
QY 640 LysIleTTPSerAlaIleLysSerTTPValThrGluTyrCysAsnTyrTyrTyrLysSer 659
Db 1953 GAAATTTGGCGAGCAATCAAAAGTTGGGTAAACAGAAATATTCGAAGTCTTATPACAAATCT 2012
QY 660 AspAspAlaValGlnLysAspThrGluLeuGlnAlaTTPTrpLysGluLeuArgGluGlu 679
Db 2013 GACGAGACAGTAGAAGAGACACTGACTCCAAAGCTTGGTGAAGAGAGCTCCGCCAAGAA 2072
QY 680 GlyHisGlyAspLysAspGluProTTPTrpProLysMetGlnThrValGlnGluLeu 699
Db 2073 GGACATGGCGACAGAAAGATGAGGCTTGGTGGCTTAACTGCAAACTCGACAAGAGCTC 2132
QY 700 IleAspSerCysThrIleThrIleTTPleAlaSerAlaLeuHisAlaValAsnPhe 719
Db 2133 AGAGATTGTGCACCATCATATATATGGTAGCTTCAGCACTTCATGCAGCACTCCATTTT 2192
QY 720 GlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMet 739
Db 2193 GGCTTATACTCTTAGCTGGTTATCTCCCTAATCCGCCCTACTTTTAAGCTGTAAATTGATG 2252
QY 740 ProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeu 759
Db 2253 CCAGAGCCAGGAAGTGTGAGTATGAAGAGCTCAAGACAAATCCAGACAAGGTATTCTCTA 2312
QY 760 LysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSer 779
Db 2313 AAAACATTTGTTCCCTCAGTTGCAATCACCTGCTGAAATTTCCATTTTGGAGGCTCTGTC 2372
QY 780 ArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTTPThrLysAsp 799
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Db 2373 AGGCATGCTTCAGATGAGTTCCTTGGACAAAGGACTCAATTGAATGACAAAGGAT 2432
QY 800 GlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGln 819
Db 2433 AAAGAACCACCTGTAGCTTTTGGAGAGGTTTGGAAAGATGCTAAGTGATATCGAGAATCGA 2492
QY 820 IleMetGlnMetAsnValAspGluLysTTPTrpLysAsnArgSerGlyProValLysValPro 839
Db 2493 ATTATGATAATGAATAGTACATAAGAGTTTGGAAAGAACAGGTGAGGCGCTTGTAAACGTTCCA 2552
QY 840 TyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSer 859
Db 2553 TATAGTTGCTCTTTCACACAGTGAAGGAGGACTCACAGGCNAAGGAATTCACCAACAGT 2612
QY 860 ValSerIle 862
Db 2613 GTGTCTATA 2621

RESULT 3
US-09-051-465-1
; Sequence 1, Application US/09051465A
; Patent No. 6355862
; GENERAL INFORMATION:
; APPLICANT: Handa, Avtar K.
; APPLICANT: Kausch, Kurt D.
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting
; FILE OF INVENTION: Production of Lipoxigenase in Fruits
; FILE REFERENCE: 7024-297
; CURRENT APPLICATION NUMBER: US/09/051,465A
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: PCT/US96/16387
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: 60/005,404
; PRIOR FILING DATE: 1995-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: ASCII
; SEQ ID NO 1
; LENGTH: 2441
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-051-465-1

Alignment Scores:
Pred. No.: 0 Length: 2441
Score: 3463.50 Matches: 650
Percent Similarity: 87.88% Conservative: 68
Best Local Similarity: 79.56% Mismatches: 94
Query Match: 76.39% Indels: 5
DB: 3 Gaps: 3

US-10-731-642A-1 (1-862) x US-09-051-465-1 (1-2441)

QY 39 SerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuSer 58
Db 2 TCAGTTGTTGATGGCAATTCCTGATTACTTGGCCAAAAGTCTCTATCCAAATGATAAGT 61
QY 59 ---SerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaIleTyr 77
Db 62 GGTTCGTGTAATTATGAT-----GGTTTGAAGGGAACCTGAGCAATCCAGCATAC 112
QY 78 LeuGluAsnTTPLeuThrAsnSerThrProIleAlaIleGlyGluSerAlaPheArgVal 97
Db 113 TTAGAGATTGGCTTACAGATCATCCCAATAACAGCAGGGGAATCAACTTTTAGTGT 172
QY 98 ThrPheAspTTPAspAspGluPheGlyValProGlyAlaPheIleIleLysAsnLeu 117
Db 173 ACATTTGACTGGATCGTGACGAGTTTGGAGTTCCAGGAGCATTCATCATCAAGATCTT 232
QY 118 HisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLys 137
Db 233 CATCTTATGATGTTCTTCTCAAGTCACTCACACTCGAAGATGTTCTCTAATATATGGA 292
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US-09-978-522-2

Alignment Scores:

Pred. No.: 0 Length: 4687
Score: 3138.00 Matches: 652
Percent Similarity: 56.19% Conservative: 110
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 69.21% Indels: 502
DB: 4 Gaps: 10

US-10-731-642A-1 (1-862) x US-09-978-522-2 (1-4687)

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QY 3 LeuGluLysIleValAspAlaThrGlyLysAspGlyLysValLysGlyThr 22
DB 13 CTTCTTTCAATGTTAGTGCCTACTCTGGGNAATGATAGAGAAATCGAGGAACT 72
QY 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42
DB 73 ATTGTGTTGATGAGAGAAATGTTGATTTTAATGACTTCAATGCACCGGTTCCGGAC 132
QY 43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuSerSerValAsnAla 62
DB 133 CGGGTTCATGAGCTTTTGGACAGGGAGTCTCTCTGCAGCTCGTCAGTCTGTTTCATGGT 192
QY 63 AspPro 64
DB 193 GATCCTGGTGAGTTTTTTTTTTTTTTTTTTTCTTCATGTTTTTGATGAGGGTGTG 252
QY 64 64
DB 253 AAGTTGGAGGAGGAGGTTGATACCGTTTGTGAGGGTGAGATGGGTTCTGAATTTGA 312
QY 64 64
DB 313 TGATAGCAATTGGAAAAAGATGTGATTTTGGAGAGGCCAAGAGGGGTTGTATTTCTCA 372
QY 64 64
DB 373 GAGATGATCAATGACTTTCTTGACATCTCCATTTCACTGGGCACATTTCTAAGTCT 432
QY 64 64
DB 433 TTTGTTTTTTGTTGTTTTTAATGCTTTTGTGTTTCTTCTCTCTGTTTATAT 492
QY 64 64
DB 493 TTTCTTTTCATCAACCACTATACATGCCACCTCAATCAATGAAATTCCTATGCAGCTG 552
QY 64 64
DB 553 CCTTTTTTTTAAGCCACTAGATCTTGGTGATTTTTTTAGTCTTAGATCTTGGGTTAGAT 612
QY 64 64
DB 613 TTCCCCAGATTTTCAAAAAAGTTGAAACTGAAATTCATAAAATTTTGGAGATCACTCCTG 672
QY 64 64
DB 673 TTGGAGTTAAAGAGAAAGAAATTTGCCATAACCAAGAGATGAATTTGTTGAAATATTTC 732
QY 64 64
DB 733 TCAAAACTTCATCAATACCTGCGCAAAACAGCCAGCTTCTGAAATTTTCATGTCAGC 792
QY 64 64
DB 793 AAAGCCACTGCTGTTGTAGCAAGTCCAAGCTCAAAACATAAAAGCTTTTCAACCCAGTG 852
QY 64 64
DB 853 ATTTTGTGAATAACATGTAATAATGTCAGTGACCTCTGTTAGTGATGATATGAACTTG 912
QY 65 -----AlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAs 80
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DB 913 TGTGCCTTTTGTAGCAAAATGGTTTACAGGGGAAACTTTGGGAAACACGATACTTTGGAAGA 972
QY 80 nTrpLeuThrAsnSerThrProIleAlaAlaGlyLysSerAlaPheArgValThrPheAs 100
DB 973 CTGGATTACCACAAATTAATCTTTTAAACCGCTGGCGAGTCTGCATTTCAAGGTCAAGTTCGA 1032
QY 100 pTrpAspAspGluPheGlyValProGlyAlaPheIleLeuLysAsnLeuHisPheSe 120
DB 1033 CTGG---GATGAGGAGATTGGAGAGCCAGGGCAATTCATATTTAGAAACAATCCACACAG 1089
QY 120 rGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPhe 140
DB 1090 TGAGTTTTTACCTCAGGACTCTCACTCTTGAAGATGTTCTCTGGACGTGGCAGAAATTCACCT 1149
QY 140 eValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAl 160
DB 1150 TGTTTGTAATTCCTGGGTCTACCCCTGCTAAGCACTACAAAACACTGACCGTGTTCCTTCC 1209
QY 160 aasn----- 161
DB 1210 TAAATCAGTAAGACTAATTTGCTTGATCTAGGAGAGTCTGCTGGCAATTTGTGGCCCAT 1269
QY 162 -----GlnAl 163
DB 1270 TGACCTTAGGCAAGAGAAATTTGCTCTAAAGGAATGTGTTTATTTTATCTGCTGCAGAC 1329
QY 163 aTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValTh 183
DB 1330 ATATCTTCCAAAGTGAACACACCCAGGGCCACTCGCGAAGTACAGAAAGGGGAACTGGTGA 1389
QY 183 rLeuArgGlyAspGlyThrGlyLysLeuGluGluTyrAspArgValTyrAspTyrAlaTy 203
DB 1390 TCTGAGGGAGATGGAACCGGAGAGCTTTAGGAATGGATCGAGTGTATGACTATGCTTA 1449
QY 203 rTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGl 223
DB 1450 CTATAATGATTTGGGGAAGCCAGACAGGAGTCTCAAAATATGCCGCCCTGTGCTGGGAGG 1509
QY 223 ySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys----- 241
DB 1510 ATCTGCAGAGTATCTTTATCCAGAGGGGAGAACTGGTAGACCAACCATCTGAAGAAAGG 1569
QY 241 ----- 241
DB 1570 TAGATATTTGATACACAAATTCATATTTGTTTCTCATGCTTTTATCATVAAAAGGATGAATA 1629
QY 242 -----ThrAspProAsnSerGluSerArgIleProLe 252
DB 1630 TGATTTGATTTCTGCTCTTCTTTTAAATTAACAGATCCCAAAACTGAGAGCAGATGCTCACT 1689
QY 252 uLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSe 272
DB 1690 TGTGATGAGCTTAAACATATATGTTCCAAAGAGATGAACGATTTGGTCACTCAAGATGTC 1749
QY 272 rAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAl 292
DB 1750 AGACTTCTGCTTATGCCCTGAAATCCATAGTTCAATCTTCTCCCTGAGTTTGAGGC 1809
QY 292 aLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGl 312
DB 1810 TCTATGTGACATCACCCCAATGATTTGACAGCTTCCAAGATGTTATAGACCTCTACGA 1869
QY 312 uGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLe 332
DB 1870 AGGAGGAATCAAGGTCCAGAGGGCCCTTTTACTGGACAAAAATTAAGGACAAATCCCTCT 1929
QY 332 uGlnIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrPr 352
DB 1930 TGAGATCTCAAGGAACCTTGTGTACCGATGGGGAACATCTCTTCAAGTTCCTCAATGCC 1989
QY 352 oGlnValIle-Gln----- 356
DB 352 oGlnValIle-Gln----- 356
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Db 1990 CCAAGTCATCAAAAGGTACTGCATACATCTTAACATCTTGTGAATCTTTTGAAGCCAGATTTAT 2049
QY 357 -----GluAspLysThrA 361
Db 2050 ATATTATTTTTCATAAAATTTGATGACGCTTTTATCATGCTGGAGCAGAGGATAAGTCTG 2109
QY 361 laTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleI 381
Db 2110 CATGAGGAGACTGACGAAGAAATTTGCTAGAGAAATGCTGCTGCACTCAACCCAGTTGTCA 2169
QY 381 leSerArg----- 383
Db 2170 TCCG-TCTACTCCAAGTAACTACAGCTTCCTTTCAAAATAATTTTAAATGCCCTGTTGT 2228
QY 383 ----- 383
Db 2229 TTTCTGAGAAATGGAACCTTGAAAGGCTTCAGACTTTGTTTCTTTCCCTCCATCTAC 2288
QY 384 -----LeuGlnGluPheProp 389
Db 2289 TGTCTAGCTCTTTTCTGATAATTTATGGCTCTTTCTACTTTGTTTGAAGGAGTTTCTCTC 2348
QY 389 roLysSerLysLeuAspProLysIleTykGlyAsnGlnAsnSerThrIleThrArgGluG 409
Db 2349 CAAAAGCAAGCTGGATCCTGAAGTTTATGGCAACCAAAACAGTTTCAATAACCAAGAAC 2408
QY 409 InIleGluAspLysLeuAspGlyLeuThrIleAspGluAla----- 422
Db 2409 ACATAGAAATCACTGATGACCTTACTATTAACAGGT-AACGCTCTTAGTTCCTGTT 2467
QY 422 ----- 422
Db 2468 CTTTCAAACTAAATTTTCAATGTCGACATGTTAATTTTTCATTTGCAATGGAAACACAGCCAT 2527
QY 423 -----IleLysThrAsnArgLeuPheIleLeuA 432
Db 2528 AGTAACGAAAAATGGTCTTTTACTAGGCAATGGAAGAAGAGGCTATTATCATATTAG 2587
QY 432 snHisAspIleLeuMetProTyLLeuArgAqIleAsnThrSerThrAspThrLysT 452
Db 2588 ATCACCATGATGTTTTCATGCATACCTTGAGGAGGATTAACACA---ACTTCCAGCAAAA 2644
QY 452 hrTyAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaI 472
Db 2645 CTTACGCTCAAGGACTCTCTCTCTCTGAAAGACGACGGAACCTTTGAAGCCACTGGCGA 2704
QY 472 leGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyT 492
Db 2705 TTGAATTGAGCCTACCAATCTTAATGGGGATAAATTCGGAGCTGTCAACAAAGTATACA 2764
QY 492 hrProAlaAspGlnGlyValGluGlySerIleTTPGlnLeuAlaLysAlaTyRAlaAlav 512
Db 2765 CACCACTGAAGATGGCGTTGAGGTTCCATTTGGCAGCTGGCTAAAGCTTATGCTGCTG 2824
QY 512 alAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeu----- 525
Db 2825 TGAATGACTCTGGCTATCATCAGCTCTCTCCAGCCACTGGTA-CGTAATCTCCCAAGGAAA 2883
QY 525 ----- 525
Db 2884 GTGCGTACAGTTGGGGCGTAAATCTGAAGCGGTTATGAATATCTTTGATGTTGGTTGCA 2943
QY 526 -----AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerA 544
Db 2944 GGTGAATACACATGCTGCAATTTAGCCATTTGATTTGCAACCAACAGGCGAGCTCAGTG 3003
QY 544 laLeuHisProIleTyRlyLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnA 564
Db 3004 TGCCTTCCCAAAATTCACAAGCTTTTGGCATCTCTCACTCCGTCGATACGATGAATATAATG 3063
QY 564 laLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThrValPheProA 584
Db 3064 CATTAGCTCGAAAAATCTCATCAATGCTGTTGGAGTGGTGGAGAGACAGTCTTTTCCAT 3123

QY 584 laLysTySerMetGluMetSerAlaValValTyLysAspTrpValPheProGluGlnA 604
Db 3124 CAAGATGATGCATGGAATGTCATCTGTTGTTTACAAAGACTGGGTTTCTCACTGAGCAAG 3183
QY 604 laLeuProThrAspLeuIleLys----- 611
Db 3184 CACTCTCTGCTGATCTCATCAA-GAGGTATATAAACTACTGTTAGTGATTGTTTCTTTTCC 3242
QY 611 ----- 611
Db 3243 TGCTGTGCAATGAATCTAGTGAATAATTGTGATTTTCACTAACTGATATGCTCCAACCTG 3302
QY 612 -----ArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeuL 628
Db 3303 GGCACCTCTTTCAGAGGAATGCGGTTGAGGATTCAGAGGCCCTCATGAGCTCCGCCCTAC 3362
QY 628 euIleGlnAspTyProTyRAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerT 648
Db 3363 TGATAGATGACTACCCCTATGCTGTTGATGACTTGAGATCTGGTCAGCTATTGAGACAT 3422
QY 648 rpValThrGluTyCysAsnTyTyTyLysSerAspAspAlaValGlnLysAspThrG 668
Db 3423 GGGTGAAGAGTATTGCTCATTTCTACTACAAGACAGATGAGATGCTCCAGAAAGACTCTG 3482
QY 668 luLeuGlnAlaTrpLysGluLeuArgGluGlyHisGlyAspLysLysAspGluP 688
Db 3483 AGCTTCAGTCTGTTGAGGAGTCAAGGAGGAGGTGATGGCAGCAAGAGGACGAGC 3542
QY 688 roTTPTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleT 708
Db 3543 CTTGGTGGCTTAAATGCTACTCTCAAGAGCTGATAGAAACATGACACCATTTATCATCT 3602
QY 708 rpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyRProTyRAlaGlyTyR 728
Db 3603 GGGTGGCTTCTGCTCTCATGCTGCTGAGTGAATTTCCGGCAGTACCTTTATGAGCTACC 3662
QY 728 euProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyR 748
Db 3663 TCCCAACCGCCCAACGATAGCCGCGAGTTCATGCTGAAGAGGCACTCTGAGTATG 3722
QY 748 luGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGlnT 768
Db 3723 AAGAACTCAAGTCAATCTCTGATAAGGCTTTCTCTGAAAAACAATCACTGCCAGCTGCAGA 3782
QY 768 hrLeuLeuGlyIleSerIleLeuSerArgHisSerSerAspThrLeuTyR 788
Db 3783 CCGTCTTGGCATCTCCCTTATTGAGTCCCTTCCAGGCATTTCTTCCGATGAGGTTTATC 3842
QY 788 euGlyGlnArgGluSerProGluTrpThrLysAspGlnGluProLeuSerAlaPheAlaA 808
Db 3843 TTGGACAGAGAGACACTCTCGAATGGACCTCGACACACACACCATTTGAAAGCTTTTGAGA 3902
QY 808 rgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluL 828
Db 3903 AATTCCGAAGGAAGCTGGCAGACATTCAGAGAAATGATCATAGATAGAAATGGAATGAGA 3962
QY 828 ysTrpLysAsnArgSerGlyProValLysValProTyRThrLeuLeuPheProThrSerG 848
Db 3963 GATTCAAGAACAGAGTTGGGCTCTGTGAAGATACCATACACACTGCTCTTACCCCAAGCG 4022
QY 848 luGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
Db 4023 AGGTGGGCTTACTGGCAAAAGGATTTCCCAACAGTGTCTCCATC 4066

RESULT 6

US-09-810-268-2
; Sequence 2, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.

; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
 ; FILE OF INVENTION: Methods of Use
 ; CURRENT APPLICATION NUMBER: US/09/810,268
 ; CURRENT FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: US 60/190,950
 ; PRIOR FILING DATE: 2000-03-21
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 2595
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; US-09-810-268-2

Alignment Scores:

Pred. No.: 3,866-301 Length: 2595
 Score: 2779.50 Matches: 525
 Percent Similarity: 74.86% Conservative: 124
 Best Local Similarity: 60.58% Mismatches: 207
 Query Match: 61.30% Indels: 11
 DB: 4 Gaps: 5

US-10-731-642A-1 (1-862) x US-09-810-268-2 (1-2595)

QY 3 LeuGluLysLeuValAspAlaThrGlyLysAspGlyLysValLysGlyThr 22
 DB 4 CTGAGCGGATCATCGCGGCTGACGGGGGGAACAGCATGCGCGCTCAAGGGCAG 63
 QY 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42
 DB 64 GTGGTCTCATCGCAGAACGTGTGGACCTCAACGACTTCGGCGCCACCGCTCGTTGAC 123
 QY 43 GlyValLeuGluPheLeuGlyArgValSerLeuLeuLeuLysSerValAsnAla 62
 DB 124 AGCATCAGCGAGTTCCTCGCAAGGGGTCACTGCGAGCTCATCAGCTCCACCTCGTTC 183
 QY 63 AspProAlaAsnGlyLeuGlnGlyArgSerLysAlaAlaThrLeuGluAsnTrpLeu 82
 DB 184 GACGCCAACACGGCAACCGCGGGGGGTGCGGGGGGAGAACCTTGAGCAGTGGCTG 243
 QY 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
 DB 244 ACGAGCTCCGCTGCTGACGACCGCGAGTCCAGTTTCGGGTCACTGCTGGGAG 303
 QY 103 AspGluGluPheGlyValProGlyAlaPheIleLeuLysAsnLeuHisPheSerGluPhe 122
 DB 304 GTGGAGAAGCTGGGAGTGGCGGGGCGTCTGCTCAAGAACCAACACCGCGCGAGTTTC 363
 QY 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisValCys 142
 DB 364 TTCTCTCAAGACATACCTCCCTGACGACGTCGCGCGCGCGCTCACTTCGTCGCG 423
 QY 143 AsnSerTrpValTrpProAlaAsnLysTrpLysSerAspArgIlePhePheAlaAsnGln 162
 DB 424 AACTCTTGGGTCTACCCCGGGGCAAGTACCGGTACACCGCGTCTTCTTCCACGAT 483
 QY 163 AlaTrpLeuProSerGluThrProAspThrLeuArgLysTrpArgGluAsnGluLeuVal 182
 DB 484 AGCTACTCTCAAGCCAGATGCGCGGGGCGTGAAGCCGTACCGCAGCAGCAGCTCCGC 543
 QY 183 ThrLeuArgGlyAspGly--ThrGlyLysLeuGluGluTrpAspArgValTrpAspTrp 201
 DB 544 AACTCTCGGGGCGACGACGACGAGGGCCCTTACAGGAGACGACCGGTGTACCGCTAC 603
 QY 202 AlaTrpTrpAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeu 221
 DB 604 GAGCTCTACACGACCTTCGGGAGCCCGAGCGGGGCAAC-----CGCGCCCATCTCTC 657
 QY 222 GlyGlySerSerGluTrpProTrpProArgArgGlyArgThrGlyArgLysProThrLys 241
 DB 658 GCGCGCTCCGCGACCAACCGCTACCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCAAC 717

QY 242 ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTrpValPro 261
 DB 718 ACCGACCCCACTCGGATAGCGACTGTCTGGAG-----CAGATCTACGTGCGG 771
 QY 262 ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281
 DB 772 CGGACGAGCGCTTCGGCCACCTCAAGATGTCGACTTCCTGGGCTACTCTCAAGGCC 831
 QY 282 IleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPhe 301
 DB 832 ATCAGCAGGACATCATCCCGCGGTGCGACGTACGTGGACACACCCCGGGCGAGTTC 891
 QY 302 AspSerPheGluAspValLeuLysLeuTrpGluGlyGlyIleLysLeuProGlnGlyPro 321
 DB 892 GACTCTTCAGGACATCATCACTGTACAGGGGCGGATCAAGTSCCAAGATCCAG 951
 QY 322 LeuLeuLysAlaIleThrAspSerIleProLeuGluLysLeuLysGluLeuLeuArgSer 341
 DB 952 CGGTCTGAGGACATCGCGCAAGCTTTCCTCGCTCGAGCTCGTCAAGGACCTCTCCCGCC 1011
 QY 342 AspGlyGluGlyLeuPheLysTrpProThrProGlnValIleGlnGluAspLysThrAla 361
 DB 1012 GCGCGGACTACCTGCTCAAGCTCCCATCCACAGATCATCCAGAGACCAAGACGG 1071
 QY 362 TrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleLe 381
 DB 1072 TGGAGGACCGACGAGGAGTTCGCGCGGAGGTGCTCGCGCGCTCAACCCGATGTGATC 1131
 QY 382 SerArgLeuGlnGluPheProLysSerLysLeuAspProLysIleTrpGlyAsnGln 401
 DB 1132 ACGCGCTTCAGGAGTTCCTCCGCAAGAGACGCTGGACCCCGCAGCAAGTACCGCGCAC 1191
 QY 402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421
 DB 1192 ACCAGCAGATCACCGCGGAGCACATCGAGAAGAACCTCGAGGGCTCAGGTGCGAGC 1251
 QY 422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTrpLeu 441
 DB 1252 GCGCTGGACGCCAACAGGCTCTACATCTGGACACACACCGCTTCATGCGTCTCTC 1311
 QY 442 ArgArgIleAsnThrSerThrAspThrLysThrTrpAlaSerArgThrLeuLeuPheLeu 461
 DB 1312 ATCGACGTCAACCACTCGAGGGCAACTTCATCTACGCCACACGACGCTCTTCTCTCG 1371
 QY 462 GlnAspAsnGlyThrLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481
 DB 1372 CGCGCGGAGCGGAGCTCGCGCTCGCATCGAGCTCAGCGCGCTACATCGACGGG 1431
 QY 482 AspGlnPheGlyAlaValSerLysValTrpProAlaAspGlnGlyValGluGlySer 501
 DB 1432 GACCTCACCGTGGCCCAAGAGCAAGTCTACACCGCGGTCCAGCGCGCTCGAGGCTGG 1491
 QY 502 IleTrpGlnLeuAlaLysAlaTrpAlaValAsnAspSerGlyValHisGlnLeuIle 521
 DB 1492 GTGTGGAGCTCGCAAGCGCTATGTGCGCGTCAACGACTCTGGGTGGCAACCACTCGTC 1551
 QY 522 SerHisTrpLeuAsnThrHisAlaIleGluProPheValIleAlaThrAsnArgGln 541
 DB 1552 AGCCACTGGCTGAACACCCCGCGGTGATGGAGCGCTTCTGATCGCGAGCAACCGGAG 1611
 QY 542 LeuSerAlaLeuHisProIleTrpLysLeuLeuHisProHisPheArgGluThrMetAsn 561
 DB 1612 CTGAGGTGACGCCCGGTGCAAGCTCTCTGAGCTCGCACTTCGCGACACCATGACC 1671
 QY 562 IleAsnAlaLeuAlaArgGlnIleLeuLeuAsnGlyGlyLeuLeuGluLeuThrVal 581
 DB 1672 ATCAACGCGCTCGCGCGGAGCGCTCATCAACCGCGCGGCGCATCTTCAGATGACCGCTC 1731
 QY 582 PheProAlaLysTrpSerMetGluMetSerAlaValValTrpLysAspTrpValPhePro 601
 DB 1732 TTCCCGGCGAGTAGCGGTGGCATGTCTCGTGGTGTACAGAGCTGGAACTTCACC 1791
 QY 602 GluGlnAlaLeuProThrAspLeuLysArgGlyValAlaValGluAspSerSerSer 621

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Db 1792 GAGCAGGGCTCCCGCCGACCTCGTCAAGAGGGCGTGGCGTGGCGACCGTCCAGC 1851
Qy 622 ProLeuGlylleArgLeuLeuGlnAspTyrProTyrAlaValAspGlyLeuYlle 641
Db 1852 CCGTCAAGTGGCGTGTGTGATCGAGGACTACCGGTACGCGAGCGACGGGTGGCCATC 1911
Qy 642 TrpSerAlaIleLysSerTrpValTrpGluTyrCysAsnTyrTyrLysSerAspAep 661
Db 1912 TGGCAGCCATCGACAGTGGGTGGGAGTACCTGGCCATCTACTACCCGACGAGCGC 1971
Qy 662 AlaValGlnLysAspThrGluLeuGlnAlaIleTrpLysGluLeuArgGluGlyHis 681
Db 1972 GCGCTGCGGGCGCAGGAGCTCGAGGCTGGTGGAGAGGAGTGGCGAGTGGGGCAC 2031
Qy 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnLysLeuLeuAep 701
Db 2032 GCGCACCACCAAGAGCGCGCCCTGGTGGCCAGATGCGAGCGCGTGTGGAGCTCCGCCAGC 2091
Qy 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaValAsnPheGlyGln 721
Db 2092 GCGTCGACCAACCATCATCTGGATCGGTGGGCTCCAGCGCGCGTGAACCTTGGGCCAG 2151
Qy 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741
Db 2152 TACCCGCTACGCGGGTACCTCCGAAACAGCGCCACGGTGAGCGCGCGGATGCCGAG 2211
Qy 742 ProGlySerProGluTyrGluLysLeuLysThrAsnProAspLysValPheLeuLysThr 761
Db 2212 CCGCGCAGCAAGAGTACAGAGTGGAGCGGAGCGCGACCCCGGAGCTTCATCCACACC 2271
Qy 762 IleThrProGlnLeuGlnThrLeuLeuGlylleSerLeuIleGluLeuLeuSerArgHis 781
Db 2272 ATCAGAGCCAGATCGAGACCATCATCTGCGCATCTGCTCATCGATCTCTTCAAGCAC 2331
Qy 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGlu 801
Db 2332 TCCTCCGACAGGTGTACTCGCGCAGCGCGACACCCCGGAGTGGACCTCCGACGCCCGG 2391
Qy 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821
Db 2392 GCGCTGGCGCGCTTCAAGAGGTTCAAGCGAGCGCGCTGGTCAAGATCGAGGGCAAGTGTG 2451
Qy 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841
Db 2452 GCGGAGAACCGGACCGCGAGTGGAGTGAAGACAGAACCGCGCCCGCGAGTTCCTCATATG 2511
Qy 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855
Db 2512 CTGCTCTATCCCAACACCTCTGACCACAGTGGCGCGCGCGAGGCTCACTGCCAAGGCG 2571
Qy 856 IleProAsnSerValSerIle 862
Db 2572 ATCCCAACAGCATCTCCATC 2592
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RESULT 7

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US-09-810-268-1
; Sequence 1, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Zea mays
US-09-810-268-1

Alignment Scores:
Pred. No.: 4,98e-301 Length: 3007
Score: 2779.50 Matches: 525
Percent Similarity: 74.86% Conservative: 124
Best Local Similarity: 60.58% Mismatches: 207
Query Match: 61.30% Indels: 11
DB: 4 Gaps: 5

US-10-731-642A-1 (1-862) x US-09-810-268-1 (1-3007)
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Qy 3 LeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysValLysGlyThr 22
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Qy 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42
Db 128 GTGGTCTCTGCGGCAAGACGTGCTGACCTCAACGACTTCGGCGCCACCGTCTGTGAC 187
Qy 43 GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerSerValAsnAla 62
Db 188 AGCATCAGCGAGTTCTCTCGCAAGGGGTCACTCGCAGCTCATCAGCTCCACCTCGTC 247
Qy 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82
Db 248 GACGCCAACCAACCGCAACCGCGGGCGGTCCGGGCGGAGCGAACTCGAGCAGTGGCTG 307
Qy 83 ThrAsnSerThrProIleAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
Db 308 ACGAGCTCGCGTCTCGTCAAGCCGCGAGTCCAAGTTCCGCTCACGTTTCGACTGGGAG 367
Qy 103 AspGluGluPheGlyValProGlyAlaPheIleLysAsnLeuHisPheSerGluPhe 122
Db 368 GTGGAGAAGCTGGGAGTTCGGGGGCGCTCGTCTGCTCAAGAACCAACACCGCCGAGTTC 427
Qy 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
Db 428 TTCTCTCAAGACAATCACCTCGACAGCTCCCGCGCGCGCGCTCACCTTCGTCGCC 487
Qy 143 AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162
Db 488 AACTCTCGGTCTACCCCGCGGCAAGTACCGCTACAACCGGCTCTTCTTCTCAACGAT 547
Qy 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182
Db 548 ACGTACCTGCCAAGCAGATCGCGCGCGCTGAAGCCGTACCGCGACGACGAGTCCGC 607
Qy 183 ThrLeuArgGlyAspGly---ThrGlyLysLeuGluGluTrpAspArgValTyrAspTyr 201
Db 608 AACCTCCCGCGCGACGACGACGAGCGGCGCTTACAGGAGCAGACCGCGGTGTACCGCTAC 667
Qy 202 AlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeu 221
Db 668 GAGCTCTACAACGACCTCGCGGAGCCCGCGCGCAAC-----CCGCGCCCTCTCTC 721
Qy 222 GlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys 241
Db 722 GCGGCTCGCGCGACACCGCTACCGCGCGCTGTCGCGCACGGGCGCAAGCCCAACAAA 781
Qy 242 ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValPro 261
Db 782 ACCGACCCCACTCGGATAGCGGACTGTCTGCTGGTGGAG-----CAGATCTACGTGCGG 835
Qy 262 ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281
Db 836 CGGACGAGCGCTTCGGCCACTCAAGATGTCGACTTCTCTGGGTACTCTCATCAAGGCC 895
Qy 282 IleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPhe 301
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896 ATCAGCAGGGCATCATCCGCGCGTGGCGACCTACGTGGACACACCCCGCGGAGTTC 955
Qy
302 AppSerPheGluAspValLeuLysLeuTyrGluGlyGlyLeuLeuProGlnGlyPro 321
Db
956 GACTCTTCCAGGACATCATCAACTGTACGAGGCGGGATCAAGCTGCCAAGATCCAG 1015
Qy
322 LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341
Db
1016 GCGCTCGAGGACATCGGCAGCTCTCCGCTCGAGCTCGTCAGGACCTCTCTCCCGCC 1075
Qy
342 AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnLysPheLysThrAla 361
Db
1076 GCGCGGAGTACCTGCTCAAGCTCCCATCCACAGATCATCAAGAGGACAAAGACGCG 1135
Qy
362 TrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIle 381
Db
1136 TGGAGGACCGACGAGGAGTTCGCGGGGAGGTGCTCGCGCGGTCAACCCGATGTGATC 1195
Qy
382 SerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGln 401
Db
1196 AGCGGCTCACGAGTTCGCGCCCAAGAGCAGCTGGACCCAGCAAGTACGGCGACAC 1255
Qy
402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421
Db
1256 ACCAGCAGCATCACGCGGAGCACATCGAGAAACCTCGAGGGCTCACGGTGCAGCAG 1315
Qy
422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIleLeuMetProTyrIle 441
Db
1316 GCGCTGGAGCGCAACAGGCTCTACATCTGGACCAACAGCCGCTTACGCGGTTCCTC 1375
Qy
442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461
Db
1376 ATCAGCTCAACAACTGGAGGCACTTCATCTAGCCACAGCAGCGCTCTCTCTCTG 1435
Qy
462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481
Db
1436 CGCGCGAGCGGAGGCTCGCGCCCTCGCATCGAGCTCAGGAGCGGTCATCATCGAG 1495
Qy
482 AspGlnPheGlyValAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501
Db
1496 GACCTCACCGTGGCGCAAGAGCTCTACACGCGCGGTCCAGCGCGGTTCGAGCGCTGG 1555
Qy
502 IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521
Db
1556 GTGTGGAGCTCGCAAGGCTATGTGCGCGTCAAGACTCTGGTGGCAGCACTCTGTC 1615
Qy
522 SerHisTrpLeuAsnThrHisAlaIleGluProPheValIleAlaThrAsnArgGln 541
Db
1616 AGCCACTGGCTGAACACCCAGCGGTGTGAGGCGGCTTCGTATCGCGAGCAACCGGCG 1675
Qy
542 LeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561
Db
1676 CTGAGCGTGACCGCGGTGCACAGCTCCCTGAGCTCGCATCTCCGCGACCACTATGACC 1735
Qy
562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuLeuLeuThrVal 581
Db
1736 ATCAACGCGCTCGCGCGGAGCGCTCATCAAGCGCGGCGGATCTTCGAGATGACGCTC 1795
Qy
582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601
Db
1796 TTCCCGGGCAAGTACGCGGTGGCATGTCTCTCGGTGTACAAAGAGCTGGAACCTTACC 1855
Qy
602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValAlaValGluAspSerSer 621
Db
1856 GAGCAGGCGCTCCCGCGGACCTCTGTCAAAGAGGGCGGTGGCGGTGGCGGACCGTCCAG 1915
Qy
622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641
Db
1916 CCGTACAGTGGCTGTGATCGAGGACTACCGGTAGCGAGCGGCTGGCCATC 1975
Qy
642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661
Db
1976 TGGCAGCCATCGAGCAGTGGGTGGCGAGTACCTGGCCATCTACTTACCCCGCAGCAGCGC 2035
pb

Qy 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHis 681
Db 2036 CGCTCGCGGCGGACGAGGAGCTGCAGGCTGGTGGAGAGGAGTGGCGAGGTTCGGGCAC 2095
Qy 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701
Db 2096 GCGACACACAGGACGCGCTGTGGGCCCAAGATGACAGGCGGTGTCGAGGTTCGCCAGC 2155
Qy 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721
Db 2156 GCCTGCACCATCATCTGATCGCTCGCGCTGCCACGCGCGCTCAACTTCGCGCAG 2215
Qy 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741
Db 2216 TACCGTACGCGGGGTACTCTCCGAACAGGCCACGCTGAGCGCGCGGATGCCGAG 2275
Qy 742 ProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLysThr 761
Db 2276 CCGGACAGAGGAGTACGAGGAGCTGGAGCGCGACCGCGGAGCGGCTTCATCCACACC 2335
Qy 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781
Db 2336 ATCAGGACCATCATCTGATCGCATCTCGCTCATCGAGATCTCTCCAAGCAC 2395
Qy 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyrTrpLysAspGlnGlu 801
Db 2396 TCCTCCGAGAGGTGTACTCGGCAGCGCGACACCCCGGAGTGACCTCCGACCGCGG 2455
Qy 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLysLeuSerAspIleGluAspGlnIleMet 821
Db 2456 CGCTGGCGGCTTCAAGAGGTTCAGCGACGCGCTGGTCAAGATCGAGGCAAGGTGTG 2515
Qy 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841
Db 2516 GCGGAGAACCGCGACCGCGAGCTGAGGAAACAGGAACGCGCGCGAGTCCCTTACATG 2575
Qy 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855
Db 2576 CTGCTCTATCCAAACACCTCTGACACAGTGGCGCGCGGAGGCTCACTGCCAAGGCGC 2635
Qy 856 IleProAsnSerValSerIle 862
Db 2636 ATCCCAACAGCATCTCCATC 2656

RESULT 8

US-09-751-687-10
; Sequence 10, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-751-687-10

Alignment Scores:
Pred. No.: 6,64e-290 Length: 2818
Score: 2680.00 Matches: 502
Percent Similarity: 73.25% Conservative: 136
Best Local Similarity: 57.63% Mismatches: 215
Query Match: 59.11% Indels: 18

DB: 4 Gaps: 7
US-10-731-642A-1 (1-862) x US-09-751-687-10 (1-2818)
QY 1 MetPheLeuGluLysIleValIlePheAlaIleThrGlyLysAspAspGlyLysValLys 20
DB 69 ATGCTGCTGGAGGGGTGATGACACCTCAGCGGGGCGAACAAGAGCGCGCGGTCAAG 128
QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40
DB 129 GGCACGGTGGTCTATGCGAAGACAGTGTGGACCTCAACAGCTTCGCGGCCACCATC 188
QY 41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuLeuLeuIleSerVal 60
DB 189 ATCGACGGCATCGCGGAGTTCCTCGCAAGGGCGTCACTGCGCAGCTTATCAGCTCCACC 248
QY 61 AsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsn 80
DB 249 GCGGTGACCAAGACACCGCGGTTCGCGGGAAGTGGCGCGGAGCGGAGCTGGAGCAG 308
QY 81 TrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAsp 100
DB 309 TGGGTGACGAGCGCTGCGGTGACGACGGGGAGTCCAAAGTTCGGCTCACCCTTCGAC 368
QY 101 TrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSer 120
DB 369 TGGGAGGTGAGAGCTCGGGGTGCGGGCGGCATCGTCTCAACACTACACAGCTCC 428
QY 121 GluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis---GlyLysValHis 139
DB 429 GAGTTCCTGCTTAAACACCATCACCTCCACGAGCTCCCGCGCGGACCACTCAC 488
QY 140 PheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhe 159
DB 489 TTCGTGCGCAACTCATGAGTACCCCGCGCAACTACCGATACAGCGCGCTCTCTTC 548
QY 160 AlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsn 179
DB 549 GCCAACGACACGTACTCGCGAGCCAGATGCGCGGGCGCTGAAGCCGTACCGCGACGAC 608
QY 180 GluLeuValThrLeuArgGlyAspGly---ThrGlyLysLeuGluGlnTrpAspArgVal 198
DB 609 GAGCTCCGGAACCTGCTGGCGACGACGACGAGGCGCGTACACGAGGACGACGCGCATC 668
QY 199 TyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyLysLeuSerArg 218
DB 669 TACCGCTACGACGTCTACAAACGACCTCGCGGAG-----GGCGCG 707
QY 219 ProValLeuGlySerSerGluTyrProTyrProArgArgGlyValThrGlyArgLys 238
DB 708 CCATCTCTCGCGGCACTCCGACCACTTACCGCGCGCGCGCGGCGGACGAGGCGCAG 767
QY 239 ProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIle 258
DB 768 CCAACGCGCAGGACCCGAGCGCTGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 821
QY 259 TyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAla 278
DB 822 TACGTGCGCGCGGAGCAGAAGTTCGCGCACTTACGAGCTCGGAGCTCTGCTGCTGCTGCT 881
QY 279 LeuLysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHis 298
DB 882 ATCAAGGCCATCAGCAGGCGATCTGCGCGCGGTGCGCACCTAGCTGGACACCAACCC 941
QY 299 AsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyLysLeuPro 318
DB 942 GCGGAGTTCGATCTCTTCAGGACATCATCAACCTCTATGAGGCGGCGCATCAAGTGC 1001
QY 319 GlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluLeuLysGluLeu 338
DB 1002 AAGGTGGCGCGCTGGAGAGCTTCGTAAGCAGATTCGCGCTCCAGCTCATCAAGGACCTC 1061
QY 339 LeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAsp 358

DB 1062 CTCCTCCGTCGCGGAGCTCCCTGCTTAAGCTCCCGTCCCATCATCATCAGGAGAC 1121
QY 359 LysThrAlaTrpArgThrAspGluPheGlyArgGluMetLeuAlaGlyValIleAsnPro 378
DB 1122 AAGCAGGCGTGGAGACCGAGAGGTTGCGACGCGGAGGTGCTCGCGCGCTCAACCG 1181
QY 379 ValIleIleSerArgLeuGlnGluPheProLysSerLysLeuAspProLysIleTyr 398
DB 1182 GTCATGATCAGCGCTCTCAGGAGTTCGCGCAAAAGTAGTCTGGACCTAGCAAGTTT 1241
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QY 419 IleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisIleAspIleLeuMet 438
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QY 439 ProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeu 458
DB 1362 CGTTCCTGATGACGTCAACAACTGCGCGGCAACTTCATCTACGCCACGAGGACCTTC 1421
QY 459 LeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHis 478
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QY 479 ProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGly--- 497
DB 1482 ATCCAGGCGCGCTTACCAACGCGCAAGAGGTTTACAGCGCGGTGCCCGCGCTCC 1541
QY 498 ValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyVal 517
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QY 518 HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla 537
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QY 538 ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg 557
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QY 578 GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp 597
DB 1782 GAGATGACGGTGTTCGCGGCAAGTTCGCGTGGGATGTCGCGCGTGTGTATACAGGAC 1841
QY 598 TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGlu 617
DB 1842 TGAAGTTTCAACGAGCAGGAGCTGCGGACGATCTCATCAAGAGGCGCATGCGGTGGAG 1901
QY 618 AspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAsp 637
DB 1902 GACCGCTCGAGCGCGCTACAGGTGCGGTGTGTGTGTCGGACTACCCGTACGCGCGGAC 1961
QY 638 GlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyr 657
DB 1962 GGGTGGCGATCTGGCAGCCATTGAGCAGTACGTGAGCGAGTACTCGGCATCTACTATC 2021
QY 658 LysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArg 677
DB 2022 CCGAACGACGCGGTGCTGCGAGGCGATACGAGGTGCGGCGTGTGTGAAGAGGAGCGCGC 2081
QY 678 GluGluGlyHisGlyAspLysAspGluProTrpTrpProLysMetGlnThrValGln 697
DB 2082 GAGTTCGGGCGCGGACCTCAAGGACCGCCCATGTTGGTGGCCCAAGATCAAGTGTGCGC 2141
QY 698 GluLeuIleAspSerCysThrIleThrIleAlaSerAlaLeuHisAlaAlaVal 717

Db 2142 GAGCTGGCCAGCGGTGCACACCATCATCTCGATCGGGTGGCGCTGCATGGCGCAGTC 2201
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Db 2202 AACTTCGGGCGAGTACCCCTACGCGGGGTTCCTCCCGAAACCGCGCAGCGTGAGCGCGGC 2261
Qy 738 PheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysVal 757
Db 2262 CGCATCGCGGAGCCCGGACGAGGAGTACGGGAGCTGGAGCGCACCCGGAGCGGCC 2321
Qy 758 PheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluile 777
Db 2322 TTATCCACACCATCACGAGCCAGATCCAGACCATCATCGGGTGTCTGCTGTGGAGGTG 2381
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Qy 818 AspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProValLys 837
Db 2502 AGCAAGGTGGTGGCATGAACCATGACCGCGAGGCTCAAGAACCGCAACCGCCCGGCTAAG 2561
Qy 838 ValProThrThrLeuLeuPhePro---ThrSerGlu-----GlyGlyLeu 851
Db 2562 TTTCCCTATACGTCTGCTTACCCCAACACCTCCGACCAAGGGCGCGCTGTCGGGGCTT 2621
Qy 852 ThrGlyLysGlyIleProAsnSerValSerIle 862
Db 2622 ACCGCCAAGGGCATCCCAACAGCATCTCCATC 2654

RESULT 9

US-09-751-687-8
; Sequence 8, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Rech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.110501
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 4663
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-751-687-8

Alignment Scores:
Pred. No.: 1.15e-244 Length: 4663
Score: 2280.50 Matches: 504
Percent Similarity: 45.89% Conservative: 138
Best Local Similarity: 36.03% Mismatches: 211
Query Match: 50.30% Indels: 548
DB: 4 Gaps: 14

US-10-731-642A-1 (1-862) x US-09-751-687-8 (1-4663)

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Qy 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40
pb 417 GGCACGGTGGTGTCTATGCGCAAGACGTGCTGGACCTCAACGACTTCGGCGCCACCATC 476

Qy 41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerSerVal 60
Db 477 ATCAGCGCATCGCGAGTTCCTCGCAAGGCGCTCACCTCCAGCTTATCAGCTCCACC 536
Qy 61 -----AsnAlaAspProAlaAsnGlyLeu----- 68
Db 537 GCCGTGCAGCAAGGTAATCACTA---CCCTCTCTCCGCGCTTCTCTCTGTTTACAAGATATA 595
Qy 68 ----- 68
Db 596 GTATTTCTTCTGTCGTGGCGCGCCCATGGATGGATGGATGGATGGATGGATGGATGGAT 655
Qy 68 ----- 68
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Qy 68 ----- 68
Db 716 AAAAGAGACAACAGCATGTCATGTCGTGGCGCACCCAGACACGACGACGACGACGATG 775
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Qy 68 ----- 68
Db 1016 CAAGCAGGTACGTGGCATGTATAGTTCCTTGTAGTAACTAAGCATGTGATGTAGAGAG 1075
Qy 69 -----GlnGlyLysArgSerLysAlaIleTyrLeuGlu 79
Db 1076 GTACGTGTGTGTCAGACAACGCGCGTCTCGGGAAGGTGGCGCGGAGCGGAGCTGGAG 1135
Qy 80 AsnTrpLeuThrAsnSerThrProIleAlaGlyGluSerAlaPheArgValThrPhe 99
Db 1136 CAGTGGGTGACGAGCTGCGCTGCTGACGCGGGGAGTCCAAAGTTCGGCTCACCTTC 1195
Qy 100 AspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPhe 119
Db 1196 GACTGGGAGGTGGAGAGCTCGGGTCCCGGCGGCATCGTCGTCACAACTACCACTACCA 1255
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Db 1256 TCCGAGTTCTCTGCTTAAACCATCACCTCCACGACGTCCTCCGCGCGCAGCGCAACCTC 1315
Qy 139 HisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhe 158
Db 1316 ACCTTCGTGCGCAACTCATGTGATCTACCCCGCGCAACTACCGATACAGCGCGGTCTTC 1375
Qy 159 PheAlaAsn----- 161
Db 1376 TTCGCCAAGCAGCGTGGAGATTTTCTCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1435
Qy 161 ----- 161
Db 1436 CGTCATTTCATGTCGATCATTAAAGTCTTTCGCCAGGACATAGATGATGATGATGATGAT 1495
Qy 161 ----- 161
Db 1496 TACCACCTTAGCAGTACGTACATTATTTATTCGTTGGTGTAGAAAAGGATATGTTGGT 1555

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162 ----- GlnAlaTyrLeuProSe 167
1976 AAACATAAATTTTATATGTAATGTTGCACGGCTCCACACTCGCAGACGTACTGCGGAG 2035
167 rGluthrProAspThrLeuArgLysTyrArgGluAsnGluValThrLeuArgGlyAs 187
2036 CCAGATGCGCGCGCGCTGAAGCCGTACCGCAGCAGCAGAGCTCCGGAACCTCGTGGCGA 2095
187 pGly---ThrGlyLysLeuGluGluTyrAspArgValTyrAspTyrAlaTyrTyrAsnAs 206
2096 CGACACGAGGCGCGTACCAGGAGCAGCAGCGCATCTACCGTAGCAGCTCTACACGA 2155
206 pLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerG1 226
2156 CCTCGCGGAG-----GGCCGCCCATCTCTCGGCGCAACTCCGA 2194
226 uTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsnSe 246
2195 CCACCTTTACCCGCGCGCGCGCAGCAGGAGCGCAAGCCCAACGCCAGCGACCCGAGCCT 2254
246 rGluSerArgLysProLeuMetSerLeuAspLysTyrValProArgAspGluArgPh 266
2255 GGAGAGCGCGCTGCTGCTGGAG-----CAGATCTAGTGGCGCGGAGCAGAGATT 2308
266 eGlyHisLysLeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLe 286
2309 CGGCCACCTCAAGACGTCGCACTCTCTGGGCTACTCCATCAAGGCCATCAGCAGGGCAT 2368
286 uLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAs 306
2369 CTGCGCGCGCGCGCATCTAGTGGACACCAACCCCGCGGAGTTGCACTCTCTCCAGGA 2428
306 pValLeuLysLeuTyrGluGlyGlyLysLeuProGlnGlyProLeuLeuLysAlaI1 326
2429 CATCATCACTCTAGAGGCGGCATCAAGTGTGCCAAGTGGCGCGCTCGAGGAGCT 2488
326 eThrAspSerIleProLeuGluLeuLeuLysGluLeuLeuArgSerAspGlyGlyLe 346
2489 CCGTAAGCAGGTTCCCGCTCCAGCTCATCAAGGACCTCTCTCCCGCTCGGCGGAGCTCCCT 2548
346 uPheLysTyrProThrProGlnValIleGlnGluAspLysThrAlaTyrArgThrAspG1 366
2549 GCTTAAGCTCCCGTCCCGCCATCTCCAGGAGCAACAGCAGGCGTGGAGGACCGACGA 2608
366 uGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeu----- 384

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384 ----- 384
Db 2669 GAGTCAGCGATTATTTGTTTCATTTGTTGTTATGTTGTTCCATGGTGAAGAGTGCAGATC 2728
385 ----- GlnGluPheProLys 391
2729 TTGATTTGGTGGTGGTCGATGCACGCGATGTCGATGATGATGATGATGATGATGATGATGAT 2788
391 erLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGlnIleG 411
2789 GTAGTCTGCAGCCCTAGCAAGTTTGGTACCACACCGACCATCAGCGCGGAGCAGCATAG 2848
411 luAspLysLeuAspGlyLeuThrIleAsp----- 420
2849 AGAAGAACCTCGAGGCGCTCAGCGTGCAGCAGGTAATTGGTCCAAAGCCATCGACATCAAC 2908
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2909 TATGATTTACCTAGGAGTAATTGGTAGCTGTAGATAATTGGCTTCGTTGCAATTAATTT 2968
421 ----- GluAlaIleLysThrAsnA 427
2969 GATGCTGGCGGATCAAGTATCGTATTGGGTTTGAATAATTGCGAGCGCTGGAAAGCAACA 3028
427 rGluPheLleLeuAsnHisAspIleLeuMetProTyrLeuArgArgIleAsnThrS 447
3029 GGCTGTATCTCTGATCACCATGACCGGTTTCATCCGTTCTGATCGACGCAACACC 3088
447 erThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrL 467
3089 TCCCCGGCAACTTCATCTACGCCACGAGACCCCTCTTCTCTCGCGGCGGAGCGAGC 3148
467 euLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaV 487
3149 TCACGCGCTCGCCATCGAGCTGAGCGAGCCCATCATCAGCGCGGCTTACCACGGCCA 3208
487 alSerLysValTyrThrProAlaAspGlnGly---ValGluGlySerIleThrGlnLeuA 506
3209 AGAGCAAGGTTTACACGCGCGTCCGCGCAGCGCTCCGTCGAAGGCTGGGTGGGAGCTCG 3268
506 laLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTsp--- 524
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524 ----- 524
3329 TTCTCCCGTCGATGTGATTGATTCAGTCAGTCGATGCACAACTCATCGAAATATGATTG 3388
525 ----- LeuAsnThrHisAlaIleGluProPheValIleAlaThrAsn 539
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540 ArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThr 559
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560 MetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeu 579
3509 ATGACCATCAACGCGTGGCGGCGAGCGCTCATCAACCGCGCGGCGCATCTTCGAGATG 3568
580 ThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpVal 599
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600 PheProGluGlnAlaLeuProThrAspLeuIleLys----- 611
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611 ----- 611

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120 SerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis---GlyLysVal 138
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139 HisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhe 158
1316 ACCTTCGTCCGCAACTCATGGATCTACCCGCGCAACTACCGATACAGCGCGCTCTTC 1375
159 PheAlaAsn----- 161
1376 TTCGCCACGACGTGGTGGATTTCCTCTACTTTCCTCTCTCTTCATTTCACCGCCTT 1435
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2036 CCAGATGCGCGCGCGCTGAAGCCGTACCGCAGCAGCAGCTCCGGAACCTCGTGGCGA 2095
187 pGly---ThrGlyLysLeuGluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsnAs 206
2096 CGACACGAGGCGCGTACCGAGACAGCAGCGCATCTACCGCTACGAGCTCAACGA 2155
206 pGluGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerG1 226
2156 CCTCGCGCAG-----GGCCGCCCTCTCTCGCGGCACTCCGA 2194
226 uTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsnSe 246
2195 CCACCTTTACCGCGCGCGCGCAGCAGGAGCGCAAGCCCAACGACGACGCGAGCT 2254

246 rGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArgAspGluArgPh 266
2255 CGAGAGCGCGTGTCTGCTGGAG-----CAGATCTACGTGCGCGGAGCAGAGATT 2308
266 eGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLe 286
2309 CGCGCACCTCAAGACGCTCGACTTCTGGGTACTTCATCAAGGCATCACCAGCGCAT 2368
286 uLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGlnPheAspSerPheGluAs 306
2369 CTTGCGCGCGTGGCGCACTACGTGGACACACCCCGCGAGTTCGACTCTCTTCAGGA 2428
306 pValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAla11 326
2429 CATCATCAACCTCTATGAGCGCGCATCAAGTGCCTCAAGGTGGCGCGCTTCAGGAGCT 2488
326 eThrAspSerIleProLeuGluIleLeuLysGluLeuArgSerAspGlyGluGlyLe 346
2489 CCGTAAGCAGTTCCCGCTCCAGCTCATCAAGGACCTCTCTCCCGTCGCGCGGACTCCCT 2548
346 uPheLysTyrProThrProGlnValIleGlnLysPheValThrAlaTyrArgThrAspGl 366
2549 GCTTAAGCTCCCGTGGCCCACTCATCCAGGAGAACAGCAGGCGTGGAGGACCGACA 2608
366 uGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeu----- 384
2609 GGAGTTCGACGGGAGGTGCTCGCCNNGTCAACCGGTTCATGATCACGCGTCTCACGT 2668
384 ----- 384
2669 GAGTCAGCGATTATTGTTTCATTGTGTGTATGTGTCTCATGTGAGAAAGTCAGATC 2728
385 -----GlnGluPheProLys 391
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391 rLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIle 411
2789 GTAGTCTGACCCCTAGCAAGTTTGTGTACACACACGACCATCAGCGGAGCAGATAG 2848
411 uAspLysLeuAspGlyLeuThrIleAsp----- 420
2849 AGAAGAACCTCGAGGCGCTCAGCGTGCAGCAGGTAATTTGGTCCAAGCCATCGACATCAAC 2908
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3029 GGTGTATACCTCTGATCACCATGACCGGTTCATCGCTTCCTGATCAGCGTCAACAAC 3088
447 eThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAsnGlyThrL 467
3089 TGCCCGGCAATTCATCTACCGCAGGAGCCCTCTCTCTCGCGCGCAGCGAGGC 3148
467 uLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaV 487
3149 TCACGCGCTCGCATCGAGCTGAGCGAGCCCATCATCCAGGCGCGCTTACCACGGCA 3208
487 alSerLysValTyrThrProAlaAspGlnGly---ValGluGlySerIleThrGlnLeuA 506
3209 AGAGCAAGGTTTACAGCGCGTGCACGCGCTCGTCCGAAGCTGGGTGGGAGCTCG 3268
506 laLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrp----- 524
3269 CCAAGGCTTACGTCGCGCTCAATGACTCCGGTGGCAGCAGCTCGTACGCCACTGTTAG 3328
524 ----- 524

Db 577 TTCACATCGAGTCATGGGTTCACTCCAAATACGATAACCCCTGAGAAAAAATATTTTC 636
Qy 160 AlaAsnGlnAlaTyrlsLeuProSerGluThrProAspThrLeuArgLysTyrlsArgGluAsn 179
Db 637 ACCGACAGTCGTACTACCGTTGGAAAGCCGACCGCACTGAAGCGCTTACGAGAGAA 696
Qy 180 GluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluThrProAspArgValTyrls 199
Db 697 GATATGGATCGCTTCGAGGAACCGCAAGGAGGAACGTAATCATTCGAGCGGATATAT 756
Qy 200 AspTyrlsAlaTyrlsAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgPro 219
Db 757 GATTATGATGTACACCATCTCGAGATCCGAGTGGAGGCTTATGATCTAGCAGCGCG 816
Qy 220 ValLeuGlyGlySerSertGluTyrlsProTyrlsProArgArgGlyArgThrGlyArgLysPro 239
Db 817 GTGCTCGGTGGCGAGACA---CATCGTACCTTAGCGGTGCGGTACTGTGTGCAAAATG 873
Qy 240 ThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrls 259
Db 874 TCCTCTAAAGATCCGTTAAACAGAAAGCAGCA-----ACTACGCTCCCTTTTAT 921
Qy 260 ValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeu 279
Db 922 GTACCTCGGATGAAGATTTTTCAGAGATAAAGAGGTGTGAACCTTTTGGAGCAAAACTTTA 981
Qy 280 LysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsn 299
Db 982 TACTCTGTGCTCATGGAGTGTACCAATGCTAGACTCAATTTGTAACAGAAAGCAAG 1041
Qy 300 GluPheAspSerPheGluAspValLeuLysLeuTyrlsGluGlyGlyIleLysLeuProGln 319
Db 1042 GGGTTTCCATTATTCACATCCATAGATTGCTTTTATATGAAGGTGTTAATGTTCTCT 1101
Qy 320 GlyPro-----LeuLeuLysAlaIleThrAspSerIle 330
Db 1102 CCTGCAATGGAATTTAAGTCTTTTACCTAGACTTGTCAAGGGGCTACTGATGCC--- 1158
Qy 331 ProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrlsPro 350
Db 1159 -----GCNAATACCGTTATCAAGTTTCAG 1182
Qy 351 ThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArg 370
Db 1183 ACCCCGAAACCATTCATGATAGACCATTCCTCATGTTCCGTGTGTAAGAGGTTCGCGCG 1242
Qy 371 GluMetLeuAlaGlyValAsnProValIleSerArgLeuGlnGluPheProLys 390
Db 1243 CAATGCTTGGCGGTATTAATCTTTGTCGCATACAAATTTGGTTACGGAATGGCCATTGATG 1302
Qy 391 SerLysLeuAspProLysIleTyrlsGlyAsnGlnAsnSerThrIleThrArgGluGlnIle 410
Db 1303 AGTAACTGGACCTTGAATCTATGACACGCTGAGTCAAGCAATTTACAAAGAGATTTGTA 1362
Qy 411 GluAspLysLeuAspGly---LeuThrIleAspGluAlaIleLysThrAsnArgLeuPhe 429
Db 1363 GAGGAAGAGATTAAGAGTTTCATGACTCTTGAGGAGGCTTTAGCACAAAGAGAGCTGTT 1422
Qy 430 IleLeuAsnHisAspIleLeuMetProTyrlsLeuArgArgIleAsnThrSerThrAsp 449
Db 1423 ATGCTGGATATCATCATGCTGCTCTTGTGCTTATGTTTAAACAAA-----ACGAGGCTGAA 1476
Qy 450 ThrLysThr---TyrlsAspArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLys 468
Db 1477 GGGAACTTTGATGTTTCAAGAACTTTAATGTTCTTACTCTGCTGGAACTTAAGG 1536
Qy 469 ProSerAlaIleGluLeuSerLeuProAspGlyAspGlnPheGlyAlaValSer 488
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Qy 489 LysValTyrlsProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAla 508
Db 1591 CATGTTTACACACCCGCTTGGGATGCTACAGGTGCTGATGGCTTTGGAAGCTAGCAAGGCT 1650

Qy 509 TyrAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHis 528
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Qy 529 AlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIle 548
Db 1711 TGTGTCACGGAACCTTACATTTATGCTACCAATCGCAACTCAGTCAATGTCATCAATT 1770
Qy 549 TyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGln 568
Db 1771 CGACGATTTCTACCTCCCTCATTTCCGTTTACACTATGCAAAATTAATTTCTAGCTAGACT 1830
Qy 569 IleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrlsSerMet 588
Db 1831 TTACTCGTCATGCCATGGGTATCATAGATCAACATTTTCTCTGGAGATTTGTATG 1890
Qy 589 GluMetSerAlaValValTyrls---LysAspTrpValPheProGluGlnAlaLeuProThr 607
Db 1891 CAAATTTCTCTGATGATATGATCAGCAATGGCGTTTGTATCATGAAGCGCTTCGGGCC 1950
Qy 608 AspLeuIleLysArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeu 627
Db 1951 GACCTAATTAGCAGGGGTATGCGGTTGAAGATCCACCCGACCATATGTTGTGTAACCTA 2010
Qy 628 LeuIleGlnAspTyrlsProTyrlsAlaValAspGlyLeuLysIleTrpSerAlaIleLysSer 647
Db 2011 ACAATCGAGGATTTACCCATATGCAAAATGATGTTTACTCATTATGATACCATTAACAA 2070
Qy 648 TrpValThrGluTyrlsCysAsnTyrlsTyrlsLysSerAspAspAlaValGlnLysAspThr 667
Db 2071 TGGGCAACTTCTTATGTCAACCACTATTACCCAGCAGCAATCTAGTGAATCTGATGAA 2130
Qy 668 GluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLysAspGlu 687
Db 2131 GAGCTTCAAGCATGCTGGAATCGAATCCGTACAGTGTGTCATGAGATGAAGAAGATGAA 2190
Qy 688 ProTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIle 707
Db 2191 CCATGTTGGCCACCAACTCAAAACCCAGATGATTTGATGGAATTTGTTCAACCATCTTG 2250
Qy 708 TrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrlsProTyrlsAlaGlyTyrls 727
Db 2251 TGGGTGACCTCTGTCTCAACATTCAGCAGTCAACTTCGGTCAATATGATTTTCGCGGTTAT 2310
Qy 728 LeuProAsnArgProThrLeuSerArgAsnPheMetPro-----GluProGlySerPro 745
Db 2311 TTCCCTAACAGCGCGACAAATTTCCAGAAACCAAAATGCCAACGAAAGACCCACAGACGAA 2370
Qy 746 GluTyrlsGluGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGln 765
Db 2371 GAATGGCAGTCGTTTAAAGCGACCCGAGATGCTTTATTTGAAATGCTTCCCATCCCAA 2430
Qy 766 LeuGlnThrLeuLeuGlyIleSerLeuIleGluLeuSerArgHisSerSerAspThr 785
Db 2431 ATCCAAGCTACAAAGTGATGGCGATTTTGGATGTTTATCAAGTCAATTCACAGATGAA 2490
Qy 786 LeuTyrlsLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGluProLeuSerAla 805
Db 2491 GAATATATCGTGTGAAATATTTAGCGCGCATGGGAGCGGAGCTGCTATATAAAGCAGCC 2550
Qy 806 PheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnVal 825
Db 2551 TTTGAGGAGTTTCCGTGGAAGGCTCAATGAGCTGGAGCAATCATAGACTCAAGGAACACG 2610
Qy 826 AspGluLysTrpLysAsnArgSerGlyProValLysValProTyrlsThrLeuPhePro 845
Db 2611 GATCCCAATTTGAAGATCGTAGTGGTGGCGGGTGGTTCCGTATCAACTTCTCAACCG 2670
Qy 846 ThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
Db 2671 TATTCTGAAAAAGGTGTGCGGGAGAGGTGTTCCAAACAGCATATCCATC 2721

RESULT 12

US-09-978-522-23

US 02 598 522 A1 ; Sequence 23, Application US/09978522

; Patent No. 6787684

; GENERAL INFORMATION:

APPLICANT: Descenzo, Richard

APPLICANT: Irelan, Nancy

TITLE OF INVENTION: Lipoxxygenase Genes From Vitis Vinifera

FILE REFERENCE: 29520/37890

; CURRENT APPLICATION NUMBER: US/09/978,522

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241

PRIOR FILING DATE: 2000-10-16

NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 23

; LENGTH: 1196

TYPE: DNA

ORGANISM: *Vitis vinifera* cv. Cabernet Sauvignon stem cDNA library

US-09-978-522-23

Alignment Scores:

Pred. No.:	1.28e-181	Length:	1196
Score:	1710.00	Matches:	311
Percent Similarity:	91.18%	Conservative:	51
Best Local Similarity:	78.34%	Mismatches:	35
Query Match:	37.72%	Indels:	1
DB:	4	Gaps:	0

US-10-731-642A-1 (1-862) x US-09-978-522-23 (1-1196)

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Qy	469	ProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSer	488
Db	67	CCGCTGGCGATTGAATTGAGCTACCAACATCTAATGGGATAAATTCGGAGCTGTCAAC	126
Qy	489	LysValTyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAla	508
Db	127	AAAGTATACACACCAGCTGAAGATCGCGTGAAGGTTCCATTGGCAGCTGCTCAAGCT	186
Qy	509	TyrAlaAlaValAsnAspSerGlyValHisGlnLeuLeuIleSerHisTrpLeuAsnThrHis	528
Db	187	TATGCTGCTGTGAATGACTCTGGCTATCATCAGCTCCTCAGCCACTGGTTGAATACACAT	246
Qy	529	AlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIle	548
Db	247	GCTGCAATTGAGCCATTGTGATTCAACCAACAGCGAGCTCAGTGTGCTTCACCCCAATT	306
Qy	549	TyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGln	568
Db	307	CACAAGCTTTTGATCTCTCACTTCGGTGATACATGAATATATAATGCATTAGCTCGACAA	366
Qy	569	IleLeuIleAsnGlyGlyLeuLeuLeuGluLeuThrValPheProAlaLysTyrSerMet	588
Db	367	ATCCTCATCAATGCTGGTGGAGTGTGGAGACAGAGTTTTCATCAAGTAGTATGCCATG	426
Qy	599	GluMetSerAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAsp	608
Db	427	GAATGTCACTGTGTTTACAAAGACTGGGTTCTCACTGAGCAAGCACTTCTGCTGAT	486
Qy	609	LeuIleLysArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeuLeu	628
Db	487	CTCATCAAGAGAGGAATGGCGGTTGAGGATTTCAGAGGCCCTCATGGAATCGCGCTTACG	546
Qy	629	IleGlnAspTyrProTyrAlaValAlaAspGlyLeuLysIleTrpSerAlaIleLysSerTrp	648
Db	547	ATAGATGACTACCCCTATGCTGT-GATGACTTGAGATCTGTTCAGCTATTGAGCATGG	605
Qy	649	ValThrGluTyrCysAsnTyrTyrTyrLysSerAspAlaValGlnLysAspThrGlu	668


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QY 565 uAlaArgGlnIleLeuIleAseNGlyGlyGlyLeuLeuGlu-----LeuThrValPh 582
Db 1224 CGACGACGAGCGCTGCTGACGAGCGGGGTGTTCAGCACTTCATCGGACGAGCGG 1283
QY 582 eProAlaLysTyrSerMetGluMetSerAlaValTyrLysAspTTPValPheProG1 602
Db 1284 CCCCACAGGGCCACTTCAGTGGGCAAGAGGGCTTCAGCGCTGACGCTGGCGGA 1343
QY 602 uGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerPr 622
Db 1344 CAACAAGCCCGTGTGTACCTGGAGCGGGCGGTGTCTG-----GACCC 1388
QY 622 oLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleT 642
Db 1389 T-----GCCGTGCTCCCACTACCGTACCGGACGAGCGCTTCGCTTGTG 1436
QY 642 pSerAlaIleLysSerTTPValThrGluTyrCysAsnTyrTyrLysSerAspAspAl 662
Db 1437 GGACCGTTCGAGGAGTACGTGGCGGCTCTCAGGCACTTCTACCGGACGATGCCGA 1496
QY 662 aValGlnLysAspThrGluLeuGlnAlaTTPTrpLysGluLeuArgGluGlyHisG1 682
Db 1497 CCTCGAGCGGACACCGAGATGCAATGTGGAGGACCTCACCGAG-----CACGG 1550
QY 682 yAspLysAspGluProTTPTrpProLysMetGlnThrValGlnGluLeuIleAspSe 702
Db 1551 GCTGCCCGTGGACAGTCCCTGCGGAGCTGCGCGCGTGCAGACCTGGTGCAT 1610
QY 702 rCysThrIleThrIleTTPAlaSerAlaLeuHisAlaValAsnPheGlyGlnTy 722
Db 1611 CCTCACCGCTCTTTCACCGTTCAGCTGAGTGCAGCACGGCGGTGTACTACTCANTA 1670
QY 722 rProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetPro---G1 741
Db 1671 CGAGCACTACGCTTTCGTACCGAATGCGCCCTGAGCATGCGCGGAGCCACCCGCCA 1730
QY 741 uProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLysTh 761
Db 1731 GAAGGGGACGTGCTGTGAGAGGATC-----CCGAGATGATTCACCAAGTC 1781
QY 761 rIleThrProGlnLeuGlnThrLeuGlyIleSerLeuIleGluIleLeuSerArgHi 781
Db 1782 C-----CAGATGCTCTGGCAGTCCCATCGCGCGGCGCTTCAGCTT 1826
QY 781 sSerSerAspThrLeuTyrLeu-----GlyGlnArgGluSerProGluTTPTh 797
Db 1827 CGGACACGACGAGGAGTACCTGCTGCAGCGGGCGCTGGCGCGAG-----GAGTACTT 1880
QY 797 rLysAspGlnGluProLeuSerAlaPheArgPheGlyLysLysLeuSerAspIleG1 817
Db 1881 CCACAAACCGGAGCTGGTGCCATCCGCGAGCGGTTCAGGAGCGCGCTCGCGGCCACG 1940
QY 817 uAspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProVally 837
Db 1941 CGAGCGGGTG-----GAGGCGCGCAACGCGGGCGCGCA 1973
QY 837 sValProTyrThrLeuLeuPhePro 845
Db 1974 GGTGCTTACACCATCTGCGTCCC 1998

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RESULT 15
US-09-902-540-1264
; Sequence 1264, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540

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; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1264
; LENGTH: 41310
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(41310)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1264

Alignment Scores:
Pred. NO.: 9.15e-50 Length: 41310
Score: 559.50 Matches: 175
Percent Similarity: 43.80% Conservative: 118
Best Local Similarity: 26.16% Mismatches: 236
Query Match: 12.34% Indels: 140
Gaps: 23
DB: 4

US-10-731-642A-1 (1-862) x US-09-902-540-1264 (1-41310)

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QY 236 GlyArgLysProThrLys-ThrAspProAsnSerGluSerArgIleProLeuLeuMet-- 254
Db 38541 GCTCGCTCGCGAGCAAGCAGCAGCGAGTCCACGCGCGCGCGAGCTGCTCGAGGC 38600
QY 255 -----SerLe 256
Db 38601 CCGCCACGGATGTACCGTGGCGCGCTCGATGACCGAGGGGTTCGCGGCGCCT 38660
QY 256 uAspIleTyr-----ValProArgAspGluArgPheGlyHisIleLysLeuSe 272
Db 38661 CGACTCCGTGAGGGAGCGCTGCGGAGGACGAGCTCTACCGGGGCTCGAGGAGGG 38720
QY 272 rAspPheLeuThrPheAlaLeuLysSerIle-----ValGlnLeuLeuProGluPh 290
Db 38721 CAGCTACGAGTGTCTATCGCAAGAGCGTGGCGGCCATCAAGCTGAACCTGCCATGCT 38780
QY 290 eLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLe 310
Db 38781 GACCGCGCTTGGAAACGGGCTGGTGGACATCTTCGACTTCTTCAACAC----- 38829
QY 310 uTyrGluGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIl 330
Db 38829 ----- 38829
QY 330 eProLeuGluIleLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrPr 350
Db 38830 -----CTGAGGTG----- 38838
QY 350 oThrProGlnValIleGlnGluAspLysThrAlaTTPArgThrAspGluGluPheGlyAr 370
Db 38839 -----CCCCAGTCCGCCAGCGC-----TGAAGGACGACCTCGAGTTCGCCGG 38882
QY 370 gGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGluPheProProLy 390
Db 38883 CGAGCGCTCCAGGGCATCGCCCCCTCCACATCAGCTCGCTCCCGCTGCTGCGC----- 38937
QY 390 sSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIl 410
Db 38938 -----CAGGGCATGCGCTCACCAGCAGCAGCT 38966
QY 410 eGluAspLysLeuAsp---GlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPh 429
Db 38967 CCGGGCGCTTGTGCGCGCACCGCTCGCGAGGGCGCTCGACGCCAAGCGATCTT 39026
QY 429 eIleLeuAsnHisHis-----AspIleLeuMetProTyrLeuArgArgIleAsnThrSe 447

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[illegible]

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